

SEQUENCE LISTING

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Hueckelhoven, Ralph

<120> METHOD FOR INCREASING RESISTANCE AGAINST STRESS FACTORS IN PLANTS

<130> 12810-00137-US

<150> PCT/EP2004/002436

<151> 2004-03-10

<150> DE 103 11 118.2

<151> 2003-03-12

<160> 63

<170> PatentIn version 3.3

<210> 1

<211> 744

<212> DNA

<213> Hordeum vulgare

<220>

<221> CDS

<222> (1) .. (741)

<223> coding for BI1-protein

<400> 1

atg	gac	gcc	ttc	tac	tcg	acc	tcg	tcg	gcg	gcg	gcg	agc	ggc	tgg	ggc	48
Met	Asp	Ala	Phe	Tyr	Ser	Thr	Ser	Ser	Ala	Ala	Ala	Ser	Gly	Trp	Gly	
1				5					10					15		

cac	gac	tcc	ctc	aag	aac	ttc	cgc	cag	atc	tcc	ccc	gcc	gtg	cag	tcc	96
His	Asp	Ser	Leu	Lys	Asn	Phe	Arg	Gln	Ile	Ser	Pro	Ala	Val	Gln	Ser	
			20					25					30			

cac	ctc	aag	ctc	gtt	tac	ctg	act	cta	tgc	ttt	gca	ctg	gcc	tca	tct	144
His	Leu	Lys	Leu	Val	Tyr	Leu	Thr	Leu	Cys	Phe	Ala	Leu	Ala	Ser	Ser	
		35					40					45				

gcc	gtg	ggt	gct	tac	cta	cac	att	gcc	ctg	aac	atc	ggc	ggg	atg	ctg	192
Ala	Val	Gly	Ala	Tyr	Leu	His	Ile	Ala	Leu	Asn	Ile	Gly	Gly	Met	Leu	
	50					55				60						

aca	atg	ctc	gct	tgt	gtc	gga	act	atc	gcc	tgg	atg	ttc	tcg	gtg	cca	240
Thr	Met	Leu	Ala	Cys	Val	Gly	Thr	Ile	Ala	Trp	Met	Phe	Ser	Val	Pro	
65					70				75					80		

gtc	tat	gag	gag	agg	aag	agg	ttt	ggg	ctg	ctg	atg	ggt	gca	gcc	ctc	288
Val	Tyr	Glu	Glu	Arg	Lys	Arg	Phe	Gly	Leu	Leu	Met	Gly	Ala	Ala	Leu	
				85				90					95			

ctg	gaa	ggg	gct	tcg	gtt	gga	cct	ctg	att	gag	ctt	gcc	ata	gac	ttt	336
Leu	Glu	Gly	Ala	Ser	Val	Gly	Pro	Leu	Ile	Glu	Leu	Ala	Ile	Asp	Phe	

100	105	110	
gac cca agc atc ctc gtg aca ggg ttt gtc gga acc gcc atc gcc ttt			384
Asp Pro Ser Ile Leu Val Thr Gly Phe Val Gly Thr Ala Ile Ala Phe			
115	120	125	
ggg tgc ttc tct ggc gcc gcc atc atc gcc aag cgc agg gag tac ctg			432
Gly Cys Phe Ser Gly Ala Ala Ile Ile Ala Lys Arg Arg Glu Tyr Leu			
130	135	140	
tac ctc ggt ggc ctg ctc tcg tct ggc ctg tcg atc ctg ctc tgg ctg			480
Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile Leu Leu Trp Leu			
145	150	155	160
cag ttt gtc acg tcc atc ttt ggc cac tcc tct ggc agc ttc atg ttt			528
Gln Phe Val Thr Ser Ile Phe Gly His Ser Ser Gly Ser Phe Met Phe			
165	170	175	
gag gtt tac ttt ggc ctg ttg atc ttc ctg ggg tac atg gtg tac gac			576
Glu Val Tyr Phe Gly Leu Leu Ile Phe Leu Gly Tyr Met Val Tyr Asp			
180	185	190	
acg cag gag atc atc gag agg gcg cac cat ggc gac atg gac tac atc			624
Thr Gln Glu Ile Ile Glu Arg Ala His His Gly Asp Met Asp Tyr Ile			
195	200	205	
aag cac gcc ctc acc ctc ttc acc gac ttt gtt gcc gtc ctc gtc cga			672
Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val Ala Val Leu Val Arg			
210	215	220	
gtc ctc atc atc atg ctc aag aac gca ggc gac aag tcg gag gac aag			720
Val Leu Ile Ile Met Leu Lys Asn Ala Gly Asp Lys Ser Glu Asp Lys			
225	230	235	240
aag aag agg aag agg ggg tcc tga			744
Lys Lys Arg Lys Arg Gly Ser			
245			

<210> 2

<211> 247

<212> PRT

<213> Hordeum vulgare

<400> 2

Met Asp Ala Phe Tyr Ser Thr Ser Ser Ala Ala Ala Ser Gly Trp Gly
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His Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro Ala Val Gln Ser
20 25 30

His Leu Lys Leu Val Tyr Leu Thr Leu Cys Phe Ala Leu Ala Ser Ser
35 40 45

Ala Val Gly Ala Tyr Leu His Ile Ala Leu Asn Ile Gly Gly Met Leu
50 55 60

Thr Met Leu Ala Cys Val Gly Thr Ile Ala Trp Met Phe Ser Val Pro
 65 70 75 80
 Val Tyr Glu Glu Arg Lys Arg Phe Gly Leu Leu Met Gly Ala Ala Leu
 85 90 95
 Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Glu Leu Ala Ile Asp Phe
 100 105 110
 Asp Pro Ser Ile Leu Val Thr Gly Phe Val Gly Thr Ala Ile Ala Phe
 115 120 125
 Gly Cys Phe Ser Gly Ala Ala Ile Ile Ala Lys Arg Arg Glu Tyr Leu
 130 135 140
 Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile Leu Leu Trp Leu
 145 150 155 160
 Gln Phe Val Thr Ser Ile Phe Gly His Ser Ser Gly Ser Phe Met Phe
 165 170 175
 Glu Val Tyr Phe Gly Leu Leu Ile Phe Leu Gly Tyr Met Val Tyr Asp
 180 185 190
 Thr Gln Glu Ile Ile Glu Arg Ala His His Gly Asp Met Asp Tyr Ile
 195 200 205
 Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val Ala Val Leu Val Arg
 210 215 220
 Val Leu Ile Ile Met Leu Lys Asn Ala Gly Asp Lys Ser Glu Asp Lys
 225 230 235 240
 Lys Lys Arg Lys Arg Gly Ser
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<210> 3

<211> 1067

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(741)

<223> coding for BI1-protein

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 1 5 10 15

tgg agc tat gat tct ctt aaa aac ttc cgt cag att tct cca gcc gtt 96
 Trp Ser Tyr Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro Ala Val
 20 25 30

cag aat cat ctt aaa cgg gtt tat ttg acc tta tgt tgt gct ctt gtg 144

Gln	Asn	His	Leu	Lys	Arg	Val	Tyr	Leu	Thr	Leu	Cys	Cys	Ala	Leu	Val
35			40							45					
gcg	tct	gcc	ttt	gga	gct	tac	ctc	cat	gtg	ctc	tgg	aat	atc	ggc	ggc
Ala	Ser	Ala	Phe	Gly	Ala	Tyr	Leu	His	Val	Leu	Trp	Asn	Ile	Gly	Gly
50			55							60					
att	ctt	aca	acg	att	gga	tgt	att	gga	act	atg	att	tgg	ctc	ctt	tca
Ile	Leu	Thr	Thr	Ile	Gly	Cys	Ile	Gly	Thr	Met	Ile	Trp	Leu	Leu	Ser
65			70							75					
tgt	cct	cct	tat	gaa	cac	caa	aaa	agg	ctt	tct	ctt	ctg	ttt	gtg	tct
Cys	Pro	Pro	Tyr	Glu	His	Gln	Lys	Arg	Leu	Ser	Leu	Leu	Phe	Val	Ser
			85							90					
gct	gtt	ctt	gaa	ggc	gct	tct	gtt	ggc	ccc	ttg	atc	aaa	gtg	gca	att
Ala	Val	Leu	Glu	Gly	Ala	Ser	Val	Gly	Pro	Leu	Ile	Lys	Val	Ala	Ile
100			105							110					
gat	gtt	gac	cca	agc	atc	ctt	atc	act	gca	ttt	gtt	gga	act	gcg	ata
Asp	Val	Asp	Pro	Ser	Ile	Leu	Ile	Thr	Ala	Phe	Val	Gly	Thr	Ala	Ile
115			120							125					
gcg	ttt	gtc	tgt	ttc	tca	gca	gca	gca	atg	tta	gca	aga	cgc	agg	gag
Ala	Phe	Val	Cys	Phe	Ser	Ala	Ala	Ala	Met	Leu	Ala	Arg	Arg	Arg	Glu
130			135							140					
tat	ctc	tac	ctt	gga	gga	ctg	ctt	tca	tct	ggc	ttg	tct	atg	cta	atg
Tyr	Leu	Tyr	Leu	Gly	Gly	Leu	Leu	Ser	Ser	Gly	Leu	Ser	Met	Leu	Met
145			150							155					
tgg	ctc	cag	ttt	gcc	tct	tca	atc	ttt	ggc	ggc	tct	gca	tct	atc	ttt
Trp	Leu	Gln	Phe	Ala	Ser	Ser	Ile	Phe	Gly	Gly	Ser	Ala	Ser	Ile	Phe
			165							170					
aag	ttt	gag	ttg	tac	ttt	gga	ctt	ttg	atc	ttt	gtg	gga	tac	atg	gtg
Lys	Phe	Glu	Leu	Tyr	Phe	Gly	Leu	Leu	Ile	Phe	Val	Gly	Tyr	Met	Val
180			185							190					
gtg	gac	aca	caa	gag	att	ata	gaa	aag	gca	cac	ctc	ggc	gac	atg	gac
Val	Asp	Thr	Gln	Glu	Ile	Ile	Glu	Lys	Ala	His	Leu	Gly	Asp	Met	Asp
195			200							205					
tat	gta	aaa	cat	tcg	ttg	acc	ctt	ttc	act	gac	ttt	gta	gct	gtg	ttt
Tyr	Val	Lys	His	Ser	Leu	Thr	Leu	Phe	Thr	Asp	Phe	Val	Ala	Val	Phe
210			215							220					
gtt	cgg	att	ctc	atc	ata	atg	ttg	aag	aac	tca	gca	gat	aaa	gaa	gag
Val	Arg	Ile	Leu	Ile	Ile	Met	Leu	Lys	Asn	Ser	Ala	Asp	Lys	Glu	Glu
225			230							235					
aag	aag	aag	aaa	agg	aga	aac	tgaggggatg	taaagttaa	ttacttttat						
Lys	Lys	Lys	Lys	Arg	Arg	Asn									
			245												
ggttgtttatc gtgtgtgtggcc acctttgaaga tattacttgt tagcactctc tatttggtgac															
831															

cagacatggt tccactaaaa aggatctgct tgtttcactt ctgcacaagt accatcttca 891
 gattgtaaat gactcgagtg ttgttcttct tttcataaac ttttgttctt taagagtttg 951
 gttctactga ttgcatctta ccaagctaag aataatgtag gaaaatgata atcctgttta 1011
 aattttctaa aatgtgtgca tttcagaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1067

<210> 4

<211> 247

<212> PRT

<213> Arabidopsis thaliana

<400> 4

Met	Asp	Ala	Phe	Ser	Ser	Phe	Phe	Asp	Ser	Gln	Pro	Gly	Ser	Arg	Ser	1	5	10	15
Trp	Ser	Tyr	Asp	Ser	Leu	Lys	Asn	Phe	Arg	Gln	Ile	Ser	Pro	Ala	Val	20	25	30	
Gln	Asn	His	Leu	Lys	Arg	Val	Tyr	Leu	Thr	Leu	Cys	Cys	Ala	Leu	Val	35	40	45	
Ala	Ser	Ala	Phe	Gly	Ala	Tyr	Leu	His	Val	Leu	Trp	Asn	Ile	Gly	Gly	50	55	60	
Ile	Leu	Thr	Thr	Ile	Gly	Cys	Ile	Gly	Thr	Met	Ile	Trp	Leu	Leu	Ser	65	70	75	
Cys	Pro	Pro	Tyr	Glu	His	Gln	Lys	Arg	Leu	Ser	Leu	Leu	Phe	Val	Ser	85	90	95	
Ala	Val	Leu	Glu	Gly	Ala	Ser	Val	Gly	Pro	Leu	Ile	Lys	Val	Ala	Ile	100	105	110	
Asp	Val	Asp	Pro	Ser	Ile	Leu	Ile	Thr	Ala	Phe	Val	Gly	Thr	Ala	Ile	115	120	125	
Ala	Phe	Val	Cys	Phe	Ser	Ala	Ala	Ala	Met	Leu	Ala	Arg	Arg	Arg	Glu	130	135	140	
Tyr	Leu	Tyr	Leu	Gly	Gly	Leu	Leu	Ser	Ser	Gly	Leu	Ser	Met	Leu	Met	145	150	155	
Trp	Leu	Gln	Phe	Ala	Ser	Ser	Ile	Phe	Gly	Gly	Ser	Ala	Ser	Ile	Phe	165	170	175	
Lys	Phe	Glu	Leu	Tyr	Phe	Gly	Leu	Leu	Ile	Phe	Val	Gly	Tyr	Met	Val	180	185	190	
Val	Asp	Thr	Gln	Glu	Ile	Ile	Glu	Lys	Ala	His	Leu	Gly	Asp	Met	Asp	195	200	205	
Tyr	Val	Lys	His	Ser	Leu	Thr	Leu	Phe	Thr	Asp	Phe	Val	Ala	Val	Phe	210	215	220	

Val Arg Ile Leu Ile Ile Met Leu Lys Asn Ser Ala Asp Lys Glu Glu
 225 230 235 240

Lys Lys Lys Lys Arg Arg Asn
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<210> 5

<211> 1160

<212> DNA

<213> Nicotiana tabacum

<220>

<221> CDS

<222> (1)..(747)

<223> coding for BI1-protein

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Met Glu Ser Cys Thr Ser Phe Phe Asn Ser Gln Ser Ala Ser Ser Arg	
1 5 10 15	
aat cgc tgg agt tac gat tct ctt aag aac ttc cgc cag atc tct ccc	96
Asn Arg Trp Ser Tyr Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro	
20 25 30	
ttt gtt caa act cat ctc aaa aag gtc tac ctt tca tta tgt tgt gct	144
Phe Val Gln Thr His Leu Lys Lys Val Tyr Leu Ser Leu Cys Cys Ala	
35 40 45	
tta gtt gct tcg gct gct gga gct tac ctt cac att ctt tgg aac att	192
Leu Val Ala Ser Ala Ala Gly Ala Tyr Leu His Ile Leu Trp Asn Ile	
50 55 60	
ggg ggc tta ctt acg aca ttg gga tgt gtg gga agc ata gtg tgg ctg	240
Gly Gly Leu Leu Thr Thr Leu Gly Cys Val Gly Ser Ile Val Trp Leu	
65 70 75 80	
atg gcg aca cct ctg tat gaa gag caa aag agg ata gca ctt ctg atg	288
Met Ala Thr Pro Leu Tyr Glu Glu Gln Lys Arg Ile Ala Leu Leu Met	
85 90 95	
gca gct gca ctg ttt aaa gga gca tct att ggt cca ctg att gaa ttg	336
Ala Ala Ala Leu Phe Lys Gly Ala Ser Ile Gly Pro Leu Ile Glu Leu	
100 105 110	
gct att gac ttt gac cca agc att gtg atc ggt gct ttt gtt ggt tgt	384
Ala Ile Asp Phe Asp Pro Ser Ile Val Ile Gly Ala Phe Val Gly Cys	
115 120 125	
gct gtg gct ttt ggt tgc ttc tca gct gct gcc atg gtg gca agg cgc	432
Ala Val Ala Phe Gly Cys Phe Ser Ala Ala Ala Met Val Ala Arg Arg	
130 135 140	
aga gag tac ttg tat ctt gga ggt ctt ctt tca tct ggt ctc tct atc	480
Arg Glu Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile	
145 150 155 160	

ctt ttc tgg ttg cac ttc gcg tcc tcc att ttt ggt ggt tct atg gcc 528
 Leu Phe Trp Leu His Phe Ala Ser Ser Ile Phe Gly Gly Ser Met Ala
 165 170 175

ttg ttc aag ttc gag gtt tat ttt ggg ctc ttg gtg ttt gtg ggc tat 576
 Leu Phe Lys Phe Glu Val Tyr Phe Gly Leu Leu Val Phe Val Gly Tyr
 180 185 190

atc att ttt gac acc caa gat ata att gag aag gca cac ctt ggg gat 624
 Ile Ile Phe Asp Thr Gln Asp Ile Ile Glu Lys Ala His Leu Gly Asp
 195 200 205

ttg gac tac gtg aag cat gct ctg acc ctc ttt aca gat ttt gtt gct 672
 Leu Asp Tyr Val Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val Ala
 210 215 220

gtt ttt gtg cga ata tta atc ata atg ctg aag aat gca tcc gac aag 720
 Val Phe Val Arg Ile Leu Ile Ile Met Leu Lys Asn Ala Ser Asp Lys
 225 230 235 240

gaa gag aag aag aag aag agg aga aac taatgcataa gcggttatcc 767
 Glu Glu Lys Lys Lys Lys Arg Arg Asn
 245

aaagactctg taactctaga atctggcatt ttcttggtca taaacttctg tagacctcg 827

acaagtatgt tgtaaatagt ttggtaacgc ctcagattaa gctgcgaggc tctgttatgc 887

cgcatgccaa tgtggttatg gtggtacata gatggttttg tttccgaagc ataccatcaa 947

ataacatgca tgtttacact atatcgataa cctacgagtg tactacttat ttctgctccc 1007

ttttgctgtg ttaggttggt catgattgta tagttgattt tccgttatgt tagaccatct 1067

tcctttcttga cgtttaattt ctcatattga tgggagaaat gaaaattcac accgtcgccc 1127

caacttgttt aagactgagg cgcaattgta gtt 1160

<210> 6

<211> 249

<212> PRT

<213> Nicotiana tabacum

<400> 6

Met Glu Ser Cys Thr Ser Phe Phe Asn Ser Gln Ser Ala Ser Ser Arg
 1 5 10 15

Asn Arg Trp Ser Tyr Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro
 20 25 30

Phe Val Gln Thr His Leu Lys Lys Val Tyr Leu Ser Leu Cys Cys Ala
 35 40 45

Leu Val Ala Ser Ala Ala Gly Ala Tyr Leu His Ile Leu Trp Asn Ile
 50 55 60

Gly Gly Leu Leu Thr Thr Leu Gly Cys Val Gly Ser Ile Val Trp Leu
 65 70 75 80
 Met Ala Thr Pro Leu Tyr Glu Glu Gln Lys Arg Ile Ala Leu Leu Met
 85 90 95
 Ala Ala Ala Leu Phe Lys Gly Ala Ser Ile Gly Pro Leu Ile Glu Leu
 100 105 110
 Ala Ile Asp Phe Asp Pro Ser Ile Val Ile Gly Ala Phe Val Gly Cys
 115 120 125
 Ala Val Ala Phe Gly Cys Phe Ser Ala Ala Ala Met Val Ala Arg Arg
 130 135 140
 Arg Glu Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile
 145 150 155 160
 Leu Phe Trp Leu His Phe Ala Ser Ser Ile Phe Gly Gly Ser Met Ala
 165 170 175
 Leu Phe Lys Phe Glu Val Tyr Phe Gly Leu Leu Val Phe Val Gly Tyr
 180 185 190
 Ile Ile Phe Asp Thr Gln Asp Ile Ile Glu Lys Ala His Leu Gly Asp
 195 200 205
 Leu Asp Tyr Val Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val Ala
 210 215 220
 Val Phe Val Arg Ile Leu Ile Ile Met Leu Lys Asn Ala Ser Asp Lys
 225 230 235 240
 Glu Glu Lys Lys Lys Lys Arg Arg Asn
 245

<210> 7

<211> 1056

<212> DNA

<213> Oryza sativa

<220>

<221> CDS

<222> (1)..(747)

<223> coding for BII-protein

<400> 7

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 1 5 10 15
 ggc tgg ggc tac gac tcg ctg aag aac ttc cgc cag atc tcc ccc gcc 96
 Gly Trp Gly Tyr Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro Ala
 20 25 30

gtc cag tcc cac ctc aag ctc gtt tac ctg aca cta tgc gtc gcc ctg 144
 Val Gln Ser His Leu Lys Leu Val Tyr Leu Thr Leu Cys Val Ala Leu
 35 40 45

gct gcg tcg gcg gtg ggc gca tac ctg cac gtc gcc ttg aac atc ggc 192
 Ala Ala Ser Ala Val Gly Ala Tyr Leu His Val Ala Leu Asn Ile Gly
 50 55 60

ggg atg ttg act atg ctc ggg tgc gtg ggg agc atc gcc tgg ttg ttc 240
 Gly Met Leu Thr Met Leu Gly Cys Val Gly Ser Ile Ala Trp Leu Phe
 65 70 75 80

tcg gtg cct gtc ttt gag gag agg aag agg ttt ggg att ctc ttg gcc 288
 Ser Val Pro Val Phe Glu Glu Arg Lys Arg Phe Gly Ile Leu Leu Ala
 85 90 95

gct gcc ctg ctg gaa ggg gct tca gtt ggg cct ctg atc aag ctt gct 336
 Ala Ala Leu Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Lys Leu Ala
 100 105 110

gta gac ttt gac tca agc att ctc gta aca gca ttt gtt gga act gcc 384
 Val Asp Phe Asp Ser Ser Ile Leu Val Thr Ala Phe Val Gly Thr Ala
 115 120 125

att gca ttt ggg tgc ttc act tgc gct gcc atc gtt gcc aag cgt agg 432
 Ile Ala Phe Gly Cys Phe Thr Cys Ala Ala Ile Val Ala Lys Arg Arg
 130 135 140

gag tac ctc tac ctt ggt ggt ttg ctc tct tct ggc ctc tcc atc ctg 480
 Glu Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile Leu
 145 150 155 160

ctc tgg ctg cag ttt gcc gca tcc atc ttt ggc cac tcc acc ggc agc 528
 Leu Trp Leu Gln Phe Ala Ala Ser Ile Phe Gly His Ser Thr Gly Ser
 165 170 175

ttc atg ttt gag gtt tac ttt ggc ctg ttg atc ttc ctg ggg tac atg 576
 Phe Met Phe Glu Val Tyr Phe Gly Leu Leu Ile Phe Leu Gly Tyr Met
 180 185 190

gtg tat gac acg cag gag atc atc gag agg gct cac cac ggt gac atg 624
 Val Tyr Asp Thr Gln Glu Ile Ile Glu Arg Ala His His Gly Asp Met
 195 200 205

gac tac atc aag cac gca ctc acc ctc ttc act gac ttc gtg gcc gtc 672
 Asp Tyr Ile Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val Ala Val
 210 215 220

ctt gtc cgg atc ctc gtc atc atg ctc aag aac gcg tct gac aag tcg 720
 Leu Val Arg Ile Leu Val Ile Met Leu Lys Asn Ala Ser Asp Lys Ser
 225 230 235 240

gag gag aag aag agg aag aag agg tct tgagagcttc tcttcccgct 767
 Glu Glu Lys Lys Arg Lys Lys Arg Ser
 245

ttgcacataa gaaaaaacca ccgcggctat tgcctctacg tattatgaca gagccgcact 827

tcaactgggt tttatgggtga atacaagttc ttttgcattt tgttgatagc gtgtgaatct 887
 tctcagggttt gtcgtcgtag tagctttgca aatactagca tgctacatga cacggatctt 947
 tctgtaatgg tggtcgcgtt gatcgaaacg tgaaaacaca tcttcatttg cgactaattt 1007
 gtttgccttt tgggtgattga tgatgatcct ttcccaaaaa aaaaaaaaaa 1056

<210> 8
 <211> 249
 <212> PRT
 <213> Oryza sativa

<400> 8
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 Gly Trp Gly Tyr Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro Ala
 20 25 30
 Val Gln Ser His Leu Lys Leu Val Tyr Leu Thr Leu Cys Val Ala Leu
 35 40 45
 Ala Ala Ser Ala Val Gly Ala Tyr Leu His Val Ala Leu Asn Ile Gly
 50 55 60
 Gly Met Leu Thr Met Leu Gly Cys Val Gly Ser Ile Ala Trp Leu Phe
 65 70 75 80
 Ser Val Pro Val Phe Glu Glu Arg Lys Arg Phe Gly Ile Leu Leu Ala
 85 90 95
 Ala Ala Leu Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Lys Leu Ala
 100 105 110
 Val Asp Phe Asp Ser Ser Ile Leu Val Thr Ala Phe Val Gly Thr Ala
 115 120 125
 Ile Ala Phe Gly Cys Phe Thr Cys Ala Ala Ile Val Ala Lys Arg Arg
 130 135 140
 Glu Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile Leu
 145 150 155 160
 Leu Trp Leu Gln Phe Ala Ala Ser Ile Phe Gly His Ser Thr Gly Ser
 165 170 175
 Phe Met Phe Glu Val Tyr Phe Gly Leu Leu Ile Phe Leu Gly Tyr Met
 180 185 190
 Val Tyr Asp Thr Gln Glu Ile Ile Glu Arg Ala His His Gly Asp Met
 195 200 205
 Asp Tyr Ile Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val Ala Val
 210 215 220

Leu Val Arg Ile Leu Val Ile Met Leu Lys Asn Ala Ser Asp Lys Ser
 225 230 235 240

Glu Glu Lys Lys Arg Lys Lys Arg Ser
 245

<210> 9

<211> 973

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)..(741)

<223> coding for BII-protein

<400> 9

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Met Asp Ser Phe Ser Ser Phe Phe Asp Ser Gln Pro Gly Ser Arg Ser	
1 5 10 15	
tgg agc tat gat tct ctc aaa aac ctc cgt cag att tct ccc tcc gtc	96
Trp Ser Tyr Asp Ser Leu Lys Asn Leu Arg Gln Ile Ser Pro Ser Val	
20 25 30	
cag aat cat ctc aag agg gtt tat ctc act ctg tgt tgt gct ctc gtt	144
Gln Asn His Leu Lys Arg Val Tyr Leu Thr Leu Cys Cys Ala Leu Val	
35 40 45	
gcg tct gcg ttt gga gct tac ctc cac gtg ctc tgg aac ata ggt ggt	192
Ala Ser Ala Phe Gly Ala Tyr Leu His Val Leu Trp Asn Ile Gly Gly	
50 55 60	
att ctc act acc att gga tgc ttt gga agc atg att tgg ctg ctc tcc	240
Ile Leu Thr Thr Ile Gly Cys Phe Gly Ser Met Ile Trp Leu Leu Ser	
65 70 75 80	
tgt cct cct tat gaa caa caa aag agg ctt tcc ctt ctg ttt ctg tct	288
Cys Pro Pro Tyr Glu Gln Gln Lys Arg Leu Ser Leu Leu Phe Leu Ser	
85 90 95	
gct gtt ctc gaa ggt gct tca gtt ggt ccc ttg atc aaa gtg gca gtt	336
Ala Val Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Lys Val Ala Val	
100 105 110	
gat ttt gac cca agc atc ctc atc act gcg ttt gtc gga act gcg ata	384
Asp Phe Asp Pro Ser Ile Leu Ile Thr Ala Phe Val Gly Thr Ala Ile	
115 120 125	
gcc ttt atc tgt ttc tca ggg gca gcg atg ttg gca aga cgc aga gag	432
Ala Phe Ile Cys Phe Ser Gly Ala Ala Met Leu Ala Arg Arg Arg Glu	
130 135 140	
tac ctc tac ctc gga gga ctg ctt tca tct ggc ttg tcc atg ctt atg	480
Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Met Leu Met	

145	150	155	160	
tgg ctt cag ttt gcc tct tcc atc ttt ggt ggc tct gca tcc atc ttt				528
Trp Leu Gln Phe Ala Ser Ser Ile Phe Gly Gly Ser Ala Ser Ile Phe				
	165	170	175	
aag ttt gag ctc tac ttt gga ctc ttg atc ttt gtg gga tac atg gtg				576
Lys Phe Glu Leu Tyr Phe Gly Leu Leu Ile Phe Val Gly Tyr Met Val				
	180	185	190	
gtg gac act caa gat att ata gag aag gcc cac ctc ggt gac atg gat				624
Val Asp Thr Gln Asp Ile Ile Glu Lys Ala His Leu Gly Asp Met Asp				
	195	200	205	
tac gtg aaa cat tcg ttg acc ctt ttc acc gat ttt gta gct gtg ttt				672
Tyr Val Lys His Ser Leu Thr Leu Phe Thr Asp Phe Val Ala Val Phe				
	210	215	220	
gtt cgt gtt ctc atc att atg ctg aag aac tcg gca gat aaa gaa gat				720
Val Arg Val Leu Ile Ile Met Leu Lys Asn Ser Ala Asp Lys Glu Asp				
	225	230	235	240
aaa aag aag agg agg agg aac tgagactaaa aagtgagaaa gaaagctaaa				771
Lys Lys Lys Arg Arg Arg Asn				
	245			
tagagtgggt gttatgtgtg tttcaaaaaa taaaaaagag tgggtgttat aagtacagac				831
atgatagcgt tgggtgttttt tacttgtttg gaacagtttt ggtaacaaca cacgttacgt				891
atttgtgtat tcctcttagt gactccagat tgtgaatgga tcagtatctt gaaactgtgt				951
tgaaaattat cagttgggag ct				973

<210> 10
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 <212> PRT
 <213> Brassica napus

<400> 10

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Gln Asn His Leu Lys Arg Val Tyr Leu Thr Leu Cys Cys Ala Leu Val				
	35	40	45	
Ala Ser Ala Phe Gly Ala Tyr Leu His Val Leu Trp Asn Ile Gly Gly				
	50	55	60	
Ile Leu Thr Thr Ile Gly Cys Phe Gly Ser Met Ile Trp Leu Leu Ser				
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Cys Pro Pro Tyr Glu Gln Gln Lys Arg Leu Ser Leu Leu Phe Leu Ser				

85										90					95						
Ala	Val	Leu	Glu	Gly	Ala	Ser	Val	Gly	Pro	Leu	Ile	Lys	Val	Ala	Val						
			100					105					110								
Asp	Phe	Asp	Pro	Ser	Ile	Leu	Ile	Thr	Ala	Phe	Val	Gly	Thr	Ala	Ile						
		115					120					125									
Ala	Phe	Ile	Cys	Phe	Ser	Gly	Ala	Ala	Met	Leu	Ala	Arg	Arg	Arg	Glu						
		130				135					140										
Tyr	Leu	Tyr	Leu	Gly	Gly	Leu	Leu	Ser	Ser	Gly	Leu	Ser	Met	Leu	Met						
145					150					155					160						
Trp	Leu	Gln	Phe	Ala	Ser	Ser	Ile	Phe	Gly	Gly	Ser	Ala	Ser	Ile	Phe						
				165					170					175							
Lys	Phe	Glu	Leu	Tyr	Phe	Gly	Leu	Leu	Ile	Phe	Val	Gly	Tyr	Met	Val						
			180					185					190								
Val	Asp	Thr	Gln	Asp	Ile	Ile	Glu	Lys	Ala	His	Leu	Gly	Asp	Met	Asp						
		195					200					205									
Tyr	Val	Lys	His	Ser	Leu	Thr	Leu	Phe	Thr	Asp	Phe	Val	Ala	Val	Phe						
		210				215					220										
Val	Arg	Val	Leu	Ile	Ile	Met	Leu	Lys	Asn	Ser	Ala	Asp	Lys	Glu	Asp						
225					230				235						240						
Lys	Lys	Lys	Arg	Arg	Arg	Asn															
				245																	

<210> 11

<211> 747

<212> DNA

<213> Glycine max

<220>

<221> CDS

<222> (1)..(744)

<223> coding for BI1-protein

<400> 11

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Arg	Leu	Gln	Ala	Met	Asp	Ala	Phe	Asn	Ser	Phe	Phe	Asp	Ser	Arg	Asn	
1				5				10					15			

cga	tgg	aat	tac	gat	act	ctc	aaa	aac	ttc	cgt	cag	att	tct	ccg	gtc	96
Arg	Trp	Asn	Tyr	Asp	Thr	Leu	Lys	Asn	Phe	Arg	Gln	Ile	Ser	Pro	Val	
			20					25					30			

gtg	cag	aat	cac	ctg	aag	cag	gtt	tat	ttt	act	ctg	tgt	ttt	gcc	gtg	144
Val	Gln	Asn	His	Leu	Lys	Gln	Val	Tyr	Phe	Thr	Leu	Cys	Phe	Ala	Val	
			35				40					45				

gtt	gct	gcg	gct	gtc	ggg	gct	tac	ctt	cat	gtc	ctc	ttg	aac	att	ggg	192
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Val	Ala	Ala	Ala	Val	Gly	Ala	Tyr	Leu	His	Val	Leu	Leu	Asn	Ile	Gly		
50						55					60						
ggt	ttt	ctt	act	aca	gtg	gca	tgc	atg	gga	agc	agc	ttt	tgg	tta	ctc	240	
Gly	Phe	Leu	Thr	Thr	Val	Ala	Cys	Met	Gly	Ser	Ser	Phe	Trp	Leu	Leu		
65					70					75					80		
tcc	aca	cct	cct	ttt	gaa	gag	agg	aag	agg	gtg	act	ttg	ttg	atg	gcc	288	
Ser	Thr	Pro	Pro	Phe	Glu	Glu	Arg	Lys	Arg	Val	Thr	Leu	Leu	Met	Ala		
				85					90						95		
gca	tca	ctg	ttt	cag	ggt	tcc	tct	att	gga	ccc	ttg	att	gat	ttg	gct	336	
Ala	Ser	Leu	Phe	Gln	Gly	Ser	Ser	Ile	Gly	Pro	Leu	Ile	Asp	Leu	Ala		
			100					105					110				
att	cat	atc	gat	cca	agc	ctt	atc	ttt	agt	gca	ttt	gtg	gga	aca	gcc	384	
Ile	His	Ile	Asp	Pro	Ser	Leu	Ile	Phe	Ser	Ala	Phe	Val	Gly	Thr	Ala		
		115					120					125					
ttg	gcc	ttt	gca	tgc	ttc	tca	gga	gca	gct	ttg	gtt	gct	agg	cgt	agg	432	
Leu	Ala	Phe	Ala	Cys	Phe	Ser	Gly	Ala	Ala	Leu	Val	Ala	Arg	Arg	Arg		
	130					135				140							
gag	tac	ctg	tac	ctt	ggt	ggc	ttg	gtt	tct	tct	gga	ttg	tcc	atc	ctt	480	
Glu	Tyr	Leu	Tyr	Leu	Gly	Gly	Leu	Val	Ser	Ser	Gly	Leu	Ser	Ile	Leu		
145					150				155						160		
ctc	tgg	ttg	cac	ttt	gct	tct	tcc	atc	ttt	gga	ggc	tca	aca	gct	ctc	528	
Leu	Trp	Leu	His	Phe	Ala	Ser	Ser	Ile	Phe	Gly	Gly	Ser	Thr	Ala	Leu		
				165					170					175			
ttt	aag	ttt	gag	ttg	tac	ttt	ggg	ctt	ttg	gtg	ttt	gta	ggt	tac	att	576	
Phe	Lys	Phe	Glu	Leu	Tyr	Phe	Gly	Leu	Leu	Val	Phe	Val	Gly	Tyr	Ile		
			180				185						190				
gta	gta	gac	acc	caa	gaa	ata	gtt	gag	agg	gca	cac	ttg	ggc	gat	ctg	624	
Val	Val	Asp	Thr	Gln	Glu	Ile	Val	Glu	Arg	Ala	His	Leu	Gly	Asp	Leu		
		195					200					205					
gac	tat	gta	aag	cat	gcc	ttg	acc	ttg	ttt	acc	gat	ttg	gtc	gca	gtt	672	
Asp	Tyr	Val	Lys	His	Ala	Leu	Thr	Leu	Phe	Thr	Asp	Leu	Val	Ala	Val		
	210					215					220						
ttt	gtc	cgg	att	ctt	gtt	att	atg	ttg	aag	aat	tcg	act	gag	agg	aat	720	
Phe	Val	Arg	Ile	Leu	Val	Ile	Met	Leu	Lys	Asn	Ser	Thr	Glu	Arg	Asn		
225					230					235					240		
gag	aag	aaa	aag	aag	aga	aga	gat	tga								747	
Glu	Lys	Lys	Lys	Lys	Arg	Arg	Asp										
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<211> 248

<212> PRT

<213> Glycine max

<400> 12

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Arg Trp Asn Tyr Asp Thr Leu Lys Asn Phe Arg Gln Ile Ser Pro Val
          20           25           30
Val Gln Asn His Leu Lys Gln Val Tyr Phe Thr Leu Cys Phe Ala Val
          35           40           45
Val Ala Ala Ala Val Gly Ala Tyr Leu His Val Leu Leu Asn Ile Gly
 50           55           60
Gly Phe Leu Thr Thr Val Ala Cys Met Gly Ser Ser Phe Trp Leu Leu
 65           70           75           80
Ser Thr Pro Pro Phe Glu Glu Arg Lys Arg Val Thr Leu Leu Met Ala
          85           90           95
Ala Ser Leu Phe Gln Gly Ser Ser Ile Gly Pro Leu Ile Asp Leu Ala
          100          105          110
Ile His Ile Asp Pro Ser Leu Ile Phe Ser Ala Phe Val Gly Thr Ala
          115          120          125
Leu Ala Phe Ala Cys Phe Ser Gly Ala Ala Leu Val Ala Arg Arg Arg
          130          135          140
Glu Tyr Leu Tyr Leu Gly Gly Leu Val Ser Ser Gly Leu Ser Ile Leu
          145          150          155          160
Leu Trp Leu His Phe Ala Ser Ser Ile Phe Gly Gly Ser Thr Ala Leu
          165          170          175
Phe Lys Phe Glu Leu Tyr Phe Gly Leu Leu Val Phe Val Gly Tyr Ile
          180          185          190
Val Val Asp Thr Gln Glu Ile Val Glu Arg Ala His Leu Gly Asp Leu
          195          200          205
Asp Tyr Val Lys His Ala Leu Thr Leu Phe Thr Asp Leu Val Ala Val
          210          215          220
Phe Val Arg Ile Leu Val Ile Met Leu Lys Asn Ser Thr Glu Arg Asn
          225          230          235          240
Glu Lys Lys Lys Lys Arg Arg Asp
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<210> 13

<211> 1510

<212> DNA

<213> Glycine max

<220>

<221> misc_feature

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 <223> n is a, c, g, or t

<220>
 <221> CDS
 <222> (1)..(777)
 <223> coding for BI-1 protein

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ttc aag tcc cca tct tct tct tct tcg aga agc cgc tgg agt tac gat	96
Phe Lys Ser Pro Ser Ser Ser Ser Ser Arg Ser Arg Trp Ser Tyr Asp	
20 25 30	
act ctc aag aat ttc cgc gag atc tct ccg ctc gtt cag aat cac atc	144
Thr Leu Lys Asn Phe Arg Glu Ile Ser Pro Leu Val Gln Asn His Ile	
35 40 45	
aaa ctg gtt tat ttt acg tta tgt tgc gct gtg gtg gct gct gct gtt	192
Lys Leu Val Tyr Phe Thr Leu Cys Cys Ala Val Val Ala Ala Ala Val	
50 55 60	
gga gct ttc ctt cat gtt ctg tgg aac att ggc ggt ttt ctc acc acg	240
Gly Ala Phe Leu His Val Leu Trp Asn Ile Gly Gly Phe Leu Thr Thr	
65 70 75 80	
ttg gct tcc att ggg agc atg ttt tgg ttg cta tct aca ccc cct ttt	288
Leu Ala Ser Ile Gly Ser Met Phe Trp Leu Leu Ser Thr Pro Pro Phe	
85 90 95	
gaa gag caa aag agg ttg tct ctg ttg atg gct tcg gcc ctg ttt cag	336
Glu Glu Gln Lys Arg Leu Ser Leu Leu Met Ala Ser Ala Leu Phe Gln	
100 105 110	
ggg gct tcc att gga cct ctg att gat ttg gct ttt gcc att gat cct	384
Gly Ala Ser Ile Gly Pro Leu Ile Asp Leu Ala Phe Ala Ile Asp Pro	
115 120 125	
ggc ctt atc att ggc gca ttt gtg gca act tct ttg gct ttt gct tgc	432
Gly Leu Ile Ile Gly Ala Phe Val Ala Thr Ser Leu Ala Phe Ala Cys	
130 135 140	
ttt tct gca gta gcc tta gtt gca agg cga agg gag tac ctc tac ctt	480
Phe Ser Ala Val Ala Leu Val Ala Arg Arg Arg Glu Tyr Leu Tyr Leu	
145 150 155 160	
ggg ggt ttg ctt tct tct tgg ctt tcc att ctt atg tgg ttg cac tct	528
Gly Gly Leu Leu Ser Ser Trp Leu Ser Ile Leu Met Trp Leu His Ser	
165 170 175	
gat tcc tct ctc ttt ggg ggc tca att gca ctc ttc aag ttt gag ctg	576
Asp Ser Ser Leu Phe Gly Gly Ser Ile Ala Leu Phe Lys Phe Glu Leu	
180 185 190	

tac ttt ggg ctt ttg gtg ttt gtg ggc tac gtt ata gta gac act caa 624
 Tyr Phe Gly Leu Leu Val Phe Val Gly Tyr Val Ile Val Asp Thr Gln
 195 200 205
 gaa att att gaa agg gct cac ttt ggt gac ctg gat tat gtg aag cat 672
 Glu Ile Ile Glu Arg Ala His Phe Gly Asp Leu Asp Tyr Val Lys His
 210 215 220
 gca ttg aca ttg ttc act gat ttg gct gca atc ttt gtg cga att ctt 720
 Ala Leu Thr Leu Phe Thr Asp Leu Ala Ala Ile Phe Val Arg Ile Leu
 225 230 235 240
 att ata atg ttg aag aat tca tct gag aga aat gag aag aag aag aaa 768
 Ile Ile Met Leu Lys Asn Ser Ser Glu Arg Asn Glu Lys Lys Lys Lys
 245 250 255
 agg aga gat tagtaggctg accgaccgac tcgagctcag gcttctctac 817
 Arg Arg Asp
 agtaatttag tttgtggaga atacataatt agctgttttag atgatgttgg tcccttgtgt 877
 agttagtttag ctatgtgttt gctgtaatgg taaatgtcag gatttctttt aaacatcttc 937
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 aataattcat ctaagagaaa tgagaagaag aggaggagag attaataaggт tgaccgattg 1297
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<211> 259

<212> PRT

<213> Glycine max

<400> 14

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Thr Leu Lys Asn Phe Arg Glu Ile Ser Pro Leu Val Gln Asn His Ile
 35 40 45
 Lys Leu Val Tyr Phe Thr Leu Cys Cys Ala Val Val Ala Ala Ala Val
 50 55 60
 Gly Ala Phe Leu His Val Leu Trp Asn Ile Gly Gly Phe Leu Thr Thr
 65 70 75 80
 Leu Ala Ser Ile Gly Ser Met Phe Trp Leu Leu Ser Thr Pro Pro Phe
 85 90 95
 Glu Glu Gln Lys Arg Leu Ser Leu Leu Met Ala Ser Ala Leu Phe Gln
 100 105 110
 Gly Ala Ser Ile Gly Pro Leu Ile Asp Leu Ala Phe Ala Ile Asp Pro
 115 120 125
 Gly Leu Ile Ile Gly Ala Phe Val Ala Thr Ser Leu Ala Phe Ala Cys
 130 135 140
 Phe Ser Ala Val Ala Leu Val Ala Arg Arg Arg Glu Tyr Leu Tyr Leu
 145 150 155 160
 Gly Gly Leu Leu Ser Ser Trp Leu Ser Ile Leu Met Trp Leu His Ser
 165 170 175
 Asp Ser Ser Leu Phe Gly Gly Ser Ile Ala Leu Phe Lys Phe Glu Leu
 180 185 190
 Tyr Phe Gly Leu Leu Val Phe Val Gly Tyr Val Ile Val Asp Thr Gln
 195 200 205
 Glu Ile Ile Glu Arg Ala His Phe Gly Asp Leu Asp Tyr Val Lys His
 210 215 220
 Ala Leu Thr Leu Phe Thr Asp Leu Ala Ala Ile Phe Val Arg Ile Leu
 225 230 235 240
 Ile Ile Met Leu Lys Asn Ser Ser Glu Arg Asn Glu Lys Lys Lys Lys
 245 250 255
 Arg Arg Asp

<210> 15
 <211> 651
 <212> DNA
 <213> Triticum aestivum

 <220>
 <221> CDS
 <222> (1)..(651)
 <223> coding for BI-1 protein

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1 5 10 15	
ctc atc tgc cgt ggg tgc tta cct gca cat tgc cct gaa cat tgg cgg	96
Leu Ile Cys Arg Gly Cys Leu Pro Ala His Cys Pro Glu His Trp Arg	
20 25 30	
gat gct gac aat gct cgc gtg tat cgg aac cat cgc ctg gat gtt ctc	144
Asp Ala Asp Asn Ala Arg Val Tyr Arg Asn His Arg Leu Asp Val Leu	
35 40 45	
ggg gcc agt cta cga gga gag gaa gag gtt tgg gct gct gat ggg tgc	192
Gly Ala Ser Leu Arg Gly Glu Glu Glu Val Trp Ala Ala Asp Gly Cys	
50 55 60	
agc ctc ctg gaa ggg gct tca gtt gga cct ctg att gag ctt gcc ata	240
Ser Leu Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Glu Leu Ala Ile	
65 70 75 80	
gac ttt gac cca agt atc ctc gtg aca ggg ttt gtc gga acc gcc atc	288
Asp Phe Asp Pro Ser Ile Leu Val Thr Gly Phe Val Gly Thr Ala Ile	
85 90 95	
gcc ttc ggg tgc ttc tct ggc gcc gcc atc atc gcc aag cgc agg gag	336
Ala Phe Gly Cys Phe Ser Gly Ala Ala Ile Ile Ala Lys Arg Arg Glu	
100 105 110	
tac ctg tac ctc ggt ggt ctg ctc tcc tcc ggc ctg tcg atc ctg ctc	384
Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile Leu Leu	
115 120 125	
tgg ctg cag ttt gcc acg tcc atc ttt ggc cac tcc tct ggc agc ttc	432
Trp Leu Gln Phe Ala Thr Ser Ile Phe Gly His Ser Ser Gly Ser Phe	
130 135 140	
atg ttt gag gtt tac ttt ggc ctg ttg atc ttc ctg gga tac atg gtg	480
Met Phe Glu Val Tyr Phe Gly Leu Leu Ile Phe Leu Gly Tyr Met Val	
145 150 155 160	
tac gac acg cag gag atc atc gag agg gcg cac cac ggc gac atg gat	528
Tyr Asp Thr Gln Glu Ile Ile Glu Arg Ala His His Gly Asp Met Asp	
165 170 175	
tac atc aag cac gcg ctc acc ctc ttc acc gac ttc gtc gcc gtt ctc	576
Tyr Ile Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val Ala Val Leu	
180 185 190	
gtc cgc gtc ctc atc atc ttg ctc aag aac gca gcg gac aag gtc gga	624
Val Arg Val Leu Ile Ile Leu Leu Lys Asn Ala Ala Asp Lys Val Gly	
195 200 205	
ggc caa gaa gag gag gaa gag aag tcc	651
Gly Gln Glu Glu Glu Glu Glu Lys Ser	
210 215	

<210> 16
 <211> 217
 <212> PRT
 <213> Triticum aestivum

<400> 16

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Asp	Ala	Asp	Asn	Ala	Arg	Val	Tyr	Arg	Asn	His	Arg	Leu	Asp	Val	Leu	35	40	45	
Gly	Ala	Ser	Leu	Arg	Gly	Glu	Glu	Glu	Val	Trp	Ala	Ala	Asp	Gly	Cys	50	55	60	
Ser	Leu	Leu	Glu	Gly	Ala	Ser	Val	Gly	Pro	Leu	Ile	Glu	Leu	Ala	Ile	65	70	75	80
Asp	Phe	Asp	Pro	Ser	Ile	Leu	Val	Thr	Gly	Phe	Val	Gly	Thr	Ala	Ile	85	90	95	
Ala	Phe	Gly	Cys	Phe	Ser	Gly	Ala	Ala	Ile	Ile	Ala	Lys	Arg	Arg	Glu	100	105	110	
Tyr	Leu	Tyr	Leu	Gly	Gly	Leu	Leu	Ser	Ser	Gly	Leu	Ser	Ile	Leu	Leu	115	120	125	
Trp	Leu	Gln	Phe	Ala	Thr	Ser	Ile	Phe	Gly	His	Ser	Ser	Gly	Ser	Phe	130	135	140	
Met	Phe	Glu	Val	Tyr	Phe	Gly	Leu	Leu	Ile	Phe	Leu	Gly	Tyr	Met	Val	145	150	155	160
Tyr	Asp	Thr	Gln	Glu	Ile	Ile	Glu	Arg	Ala	His	His	Gly	Asp	Met	Asp	165	170	175	
Tyr	Ile	Lys	His	Ala	Leu	Thr	Leu	Phe	Thr	Asp	Phe	Val	Ala	Val	Leu	180	185	190	
Val	Arg	Val	Leu	Ile	Ile	Leu	Leu	Lys	Asn	Ala	Ala	Asp	Lys	Val	Gly	195	200	205	
Gly	Gln	Glu	Glu	Glu	Glu	Glu	Lys	Ser	210	215									

<210> 17
 <211> 412
 <212> DNA
 <213> Zea mays

<220>
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 <222> (3)..(410)

<223> coding for BI1-protein

<400> 17

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acc gca gtt gct ttt gca tgc ttc tct ggc gct gcc atc atc gcc aag      95
Thr Ala Val Ala Phe Ala Cys Phe Ser Gly Ala Ala Ile Ile Ala Lys
           20             25             30

cgc agg gaa tac ctg tac ctc ggc ggt ctg ctt tca tct ggc ctc tcc      143
Arg Arg Glu Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser
           35             40             45

att ctt ctc tgg ctg cag ttt gct act tca atc ttt ggc cac acc agc      191
Ile Leu Leu Trp Leu Gln Phe Ala Thr Ser Ile Phe Gly His Thr Ser
           50             55             60

gcg acc ttc atg ttt gag ctc tac ttt ggc ctc ctg gtt ttc ctg gga      239
Ala Thr Phe Met Phe Glu Leu Tyr Phe Gly Leu Leu Val Phe Leu Gly
           65             70             75

tat atg gtg ttt gac acc cag gag atc atc gag agg gcg cac cgt ggg      287
Tyr Met Val Phe Asp Thr Gln Glu Ile Ile Glu Arg Ala His Arg Gly
           80             85             90             95

gac atg gac tac atc aag cac gcg ctg act ctc ttc acc gac ttt gtt      335
Asp Met Asp Tyr Ile Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val
           100            105            110

gcg gtt ctt gtt cga atc ctt gtc atc atg atg aag aat gca cag gag      383
Ala Val Leu Val Arg Ile Leu Val Ile Met Met Lys Asn Ala Gln Glu
           115            120            125

aaa tcc caa gac gag aag aag agg aag aa                                412
Lys Ser Gln Asp Glu Lys Lys Arg Lys
           130            135

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<210> 18

<211> 136

<212> PRT

<213> Zea mays

<400> 18

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Val Ile Asp Leu Asp Ser Arg Ile Leu Val Thr Ala Phe Val Gly Thr
   1             5             10             15

Ala Val Ala Phe Ala Cys Phe Ser Gly Ala Ala Ile Ile Ala Lys Arg
           20             25             30

Arg Glu Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile
           35             40             45

Leu Leu Trp Leu Gln Phe Ala Thr Ser Ile Phe Gly His Thr Ser Ala
           50             55             60

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Thr Phe Met Phe Glu Leu Tyr Phe Gly Leu Leu Val Phe Leu Gly Tyr
 65 70 75 80
 Met Val Phe Asp Thr Gln Glu Ile Ile Glu Arg Ala His Arg Gly Asp
 85 90 95
 Met Asp Tyr Ile Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val Ala
 100 105 110
 Val Leu Val Arg Ile Leu Val Ile Met Met Lys Asn Ala Gln Glu Lys
 115 120 125
 Ser Gln Asp Glu Lys Lys Arg Lys
 130 135

<210> 19
 <211> 345
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> CDS
 <222> (1)..(342)

<400> 19
 gcc gcc atc atc gcc aag cgc agg gag tac ctg tac ctc ggt ggc ctg 48
 Ala Ala Ile Ile Ala Lys Arg Arg Glu Tyr Leu Tyr Leu Gly Gly Leu
 1 5 10 15
 ctc tcc tcc ggc ctg tcg atc ctg ctc tgg ctg cag ttt gcc acg tcc 96
 Leu Ser Ser Gly Leu Ser Ile Leu Leu Trp Leu Gln Phe Ala Thr Ser
 20 25 30
 atc ttt ggc cac tcc tct ggc agc ttc atg ttt gag gtt tac ttt ggc 144
 Ile Phe Gly His Ser Ser Gly Ser Phe Met Phe Glu Val Tyr Phe Gly
 35 40 45
 ctg ttg atc ttt ctg gga tac atg gtg tac gac acg cag gag atc atc 192
 Leu Leu Ile Phe Leu Gly Tyr Met Val Tyr Asp Thr Gln Glu Ile Ile
 50 55 60
 gag agg gcg cac cac ggc gac atg gac tac atc aag cac gcg ctc acc 240
 Glu Arg Ala His His Gly Asp Met Asp Tyr Ile Lys His Ala Leu Thr
 65 70 75 80
 ctc ttc acc gac ttt gtc gcc gtc ctc gtc cgg atc ctc atc atc atg 288
 Leu Phe Thr Asp Phe Val Ala Val Leu Val Arg Ile Leu Ile Ile Met
 85 90 95
 ctc aag aac gca ggc gac aag tcg gag gac aag aag aag agg aag agg 336
 Leu Lys Asn Ala Gly Asp Lys Ser Glu Asp Lys Lys Lys Arg Lys Arg
 100 105 110
 agg tcc tga 345
 Arg Ser

<210> 20
 <211> 114
 <212> PRT
 <213> Triticum aestivum

<400> 20
 Ala Ala Ile Ile Ala Lys Arg Arg Glu Tyr Leu Tyr Leu Gly Gly Leu
 1 5 10 15
 Leu Ser Ser Gly Leu Ser Ile Leu Leu Trp Leu Gln Phe Ala Thr Ser
 20 25 30
 Ile Phe Gly His Ser Ser Gly Ser Phe Met Phe Glu Val Tyr Phe Gly
 35 40 45
 Leu Leu Ile Phe Leu Gly Tyr Met Val Tyr Asp Thr Gln Glu Ile Ile
 50 55 60
 Glu Arg Ala His His Gly Asp Met Asp Tyr Ile Lys His Ala Leu Thr
 65 70 75 80
 Leu Phe Thr Asp Phe Val Ala Val Leu Val Arg Ile Leu Ile Ile Met
 85 90 95
 Leu Lys Asn Ala Gly Asp Lys Ser Glu Asp Lys Lys Lys Arg Lys Arg
 100 105 110
 Arg Ser

<210> 21
 <211> 403
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (1)..(402)
 <223> coding for B11-protein

<400> 21
 ggc agc atc gcc tgg ctc ttc tcg gtg ccc gtc tac gag gag agg aag 48
 Gly Ser Ile Ala Trp Leu Phe Ser Val Pro Val Tyr Glu Glu Arg Lys
 1 5 10 15
 agg tac tgg ctg ctg atg gcg gct gcc ctc ctg gaa ggg gcg tcg gtt 96
 Arg Tyr Trp Leu Leu Met Ala Ala Ala Leu Leu Glu Gly Ala Ser Val
 20 25 30
 gga ccc ctc atc aag ctc gcc gtg gaa ttt gac cca agc atc ctg gtg 144
 Gly Pro Leu Ile Lys Leu Ala Val Glu Phe Asp Pro Ser Ile Leu Val
 35 40 45

aca gcg ttc gtg ggg act gcc att gcg ttc gcg tgc ttc tct tgc gcg 192
 Thr Ala Phe Val Gly Thr Ala Ile Ala Phe Ala Cys Phe Ser Cys Ala
 50 55 60

gcc atg gtg gcc aag cgc agg gag tac ctc tac ctg ggc ggg ctg ctc 240
 Ala Met Val Ala Lys Arg Arg Glu Tyr Leu Tyr Leu Gly Gly Leu Leu
 65 70 75 80

tct tct ggc ctc tcc atc ctg ctc tgg ctg cag ttc gcc gcc tcc atc 288
 Ser Ser Gly Leu Ser Ile Leu Leu Trp Leu Gln Phe Ala Ala Ser Ile
 85 90 95

ttc ggc cac caa tcc act agc agc ttc atg ttt gag gtc tac ttt ggg 336
 Phe Gly His Gln Ser Thr Ser Ser Phe Met Phe Glu Val Tyr Phe Gly
 100 105 110

ctg ctc atc ttc ctg ggc tac atg gtg tac gac acg cag gag gtc atc 384
 Leu Leu Ile Phe Leu Gly Tyr Met Val Tyr Asp Thr Gln Glu Val Ile
 115 120 125

gag agg gcg cac cac ggc g 403
 Glu Arg Ala His His Gly
 130

<210> 22
 <211> 134
 <212> PRT
 <213> Zea mays

<400> 22
 Gly Ser Ile Ala Trp Leu Phe Ser Val Pro Val Tyr Glu Glu Arg Lys
 1 5 10 15

Arg Tyr Trp Leu Leu Met Ala Ala Ala Leu Leu Glu Gly Ala Ser Val
 20 25 30

Gly Pro Leu Ile Lys Leu Ala Val Glu Phe Asp Pro Ser Ile Leu Val
 35 40 45

Thr Ala Phe Val Gly Thr Ala Ile Ala Phe Ala Cys Phe Ser Cys Ala
 50 55 60

Ala Met Val Ala Lys Arg Arg Glu Tyr Leu Tyr Leu Gly Gly Leu Leu
 65 70 75 80

Ser Ser Gly Leu Ser Ile Leu Leu Trp Leu Gln Phe Ala Ala Ser Ile
 85 90 95

Phe Gly His Gln Ser Thr Ser Ser Phe Met Phe Glu Val Tyr Phe Gly
 100 105 110

Leu Leu Ile Phe Leu Gly Tyr Met Val Tyr Asp Thr Gln Glu Val Ile
 115 120 125

Glu Arg Ala His His Gly
 130

<210> 23
 <211> 410
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (3)..(410)
 <223> coding for BII-protein

<400> 23

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gc tgg aac atc ggc gtg agg ctg aca atg ctc ggt tgc atc ggc agc 47
  Trp Asn Ile Gly Val Arg Leu Thr Met Leu Gly Cys Ile Gly Ser
    1             5             10             15

atc gac tgg ctc ttc tcg gtg ccc gtc tac gag gag agg aag agg tat 95
Ile Asp Trp Leu Phe Ser Val Pro Val Tyr Glu Glu Arg Lys Arg Tyr
          20             25             30

ggg ctg ctg atg gcg gct gcc ctc ctg gaa ggc gct tcg gtc gga ccc 143
Gly Leu Leu Met Ala Ala Ala Leu Leu Glu Gly Ala Ser Val Gly Pro
          35             40             45

ctc gtc aag ctc gcc gtg gaa ttt gac cca agc atc ctg gtg acg gcg 191
Leu Val Lys Leu Ala Val Glu Phe Asp Pro Ser Ile Leu Val Thr Ala
          50             55             60

ttc gtg ggg act gcc atc gcg ttc gcg tgc ttc tcc ggc gcg gcc atg 239
Phe Val Gly Thr Ala Ile Ala Phe Ala Cys Phe Ser Gly Ala Ala Met
          65             70             75

gtg gcc agg cgc agg gag tac ctc tac ctg ggc ggc ctg ctc tcg tcg 287
Val Ala Arg Arg Arg Glu Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser
          80             85             90             95

ggg ctc tcc atc ctg ctc tgg ctg cag ctc gcc gcc tcc atc ttc ggc 335
Gly Leu Ser Ile Leu Leu Trp Leu Gln Leu Ala Ala Ser Ile Phe Gly
          100             105             110

cac tcc gca acc agc ttc atg ttc gag gtc tac ttc ggg ctg ctc atc 383
His Ser Ala Thr Ser Phe Met Phe Glu Val Tyr Phe Gly Leu Leu Ile
          115             120             125

ttc ctg ggc tac gtg gtg tac gac acg 410
Phe Leu Gly Tyr Val Val Tyr Asp Thr
          130             135
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<210> 24
 <211> 136
 <212> PRT
 <213> Zea mays

<400> 24

Trp Asn Ile Gly Val Arg Leu Thr Met Leu Gly Cys Ile Gly Ser Ile

1	5	10	15
Asp Trp Leu Phe Ser Val Pro Val Tyr Glu Glu Arg Lys Arg Tyr Gly	20	25	30
Leu Leu Met Ala Ala Ala Leu Leu Glu Gly Ala Ser Val Gly Pro Leu	35	40	45
Val Lys Leu Ala Val Glu Phe Asp Pro Ser Ile Leu Val Thr Ala Phe	50	55	60
Val Gly Thr Ala Ile Ala Phe Ala Cys Phe Ser Gly Ala Ala Met Val	65	70	75
Ala Arg Arg Arg Glu Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly	85	90	95
Leu Ser Ile Leu Leu Trp Leu Gln Leu Ala Ala Ser Ile Phe Gly His	100	105	110
Ser Ala Thr Ser Phe Met Phe Glu Val Tyr Phe Gly Leu Leu Ile Phe	115	120	125
Leu Gly Tyr Val Val Tyr Asp Thr	130	135	

<210> 25

<211> 463

<212> DNA

<213> Triticum aestivum

<220>

<221> CDS

<222> (1) .. (462)

<223> coding for B11-protein

<400> 25

ttc tca ggt acg ttc cgc aat tcc cgg agc gac gat ttc gtg ctc tgc	48
Phe Ser Gly Thr Phe Arg Asn Ser Arg Ser Asp Asp Phe Val Leu Cys	
1 5 10 15	

gaa ctt cag cga gag ctc ccc cga tgc cgg gac gca acc ttg acg gtc	96
Glu Leu Gln Arg Glu Leu Pro Arg Cys Arg Asp Ala Thr Leu Thr Val	
20 25 30	

gta tac gtg atc cca ata gtg ggc cga ata aaa tct gcc gcg ggt gct	144
Val Tyr Val Ile Pro Ile Val Gly Arg Ile Lys Ser Ala Ala Gly Ala	
35 40 45	

tac ctg cac att gcc ctg aac atc ggt ggg atg ctg aca atg ctt gcg	192
Tyr Leu His Ile Ala Leu Asn Ile Gly Gly Met Leu Thr Met Leu Ala	
50 55 60	

tgt atc gga acc att gcc tgg atg ttc tct gtg cca gtc tat gag gag	240
Cys Ile Gly Thr Ile Ala Trp Met Phe Ser Val Pro Val Tyr Glu Glu	
65 70 75 80	

agg aag agg ttt ggg ctg ctg atg ggt gca gcc ctc ctg gaa ggg gct 288
 Arg Lys Arg Phe Gly Leu Leu Met Gly Ala Ala Leu Leu Glu Gly Ala
 85 90 95

tcg gtt gga cct ctg att gag ctt gcc ata gac ttt gac cca agc atc 336
 Ser Val Gly Pro Leu Ile Glu Leu Ala Ile Asp Phe Asp Pro Ser Ile
 100 105 110

ctc gtg aca ggg ttt gtt gga acc gcc atc gcc ttt ggg tgc ttc tct 384
 Leu Val Thr Gly Phe Val Gly Thr Ala Ile Ala Phe Gly Cys Phe Ser
 115 120 125

ggc gcc gcc atc atc gcc aag cgc agg gag tac ctg tac ctc gga ggc 432
 Gly Ala Ala Ile Ile Ala Lys Arg Arg Glu Tyr Leu Tyr Leu Gly Gly
 130 135 140

ctg ctc tcc tcc ggc ctg acg atc ctg ctc t 463
 Leu Leu Ser Ser Gly Leu Thr Ile Leu Leu
 145 150

<210> 26

<211> 154

<212> PRT

<213> Triticum aestivum

<400> 26

Phe Ser Gly Thr Phe Arg Asn Ser Arg Ser Asp Asp Phe Val Leu Cys
 1 5 10 15

Glu Leu Gln Arg Glu Leu Pro Arg Cys Arg Asp Ala Thr Leu Thr Val
 20 25 30

Val Tyr Val Ile Pro Ile Val Gly Arg Ile Lys Ser Ala Ala Gly Ala
 1 35 40 45

Tyr Leu His Ile Ala Leu Asn Ile Gly Gly Met Leu Thr Met Leu Ala
 50 55 60

Cys Ile Gly Thr Ile Ala Trp Met Phe Ser Val Pro Val Tyr Glu Glu
 65 70 75 80

Arg Lys Arg Phe Gly Leu Leu Met Gly Ala Ala Leu Leu Glu Gly Ala
 85 90 95

Ser Val Gly Pro Leu Ile Glu Leu Ala Ile Asp Phe Asp Pro Ser Ile
 100 105 110

Leu Val Thr Gly Phe Val Gly Thr Ala Ile Ala Phe Gly Cys Phe Ser
 115 120 125

Gly Ala Ala Ile Ile Ala Lys Arg Arg Glu Tyr Leu Tyr Leu Gly Gly
 130 135 140

Leu Leu Ser Ser Gly Leu Thr Ile Leu Leu
 145 150

<210> 27
 <211> 388
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (3)..(386)
 <223> coding for BII-protein

<400> 27
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 Trp Asn Ile Gly Gly Thr Leu Thr Met Leu Gly Cys Val Gly Ser
 1 5 10 15
 atc gcc tgg ctc ttc tcg gtg ccc gtc tac gag gag agg aag agg tat 95
 Ile Ala Trp Leu Phe Ser Val Pro Val Tyr Glu Glu Arg Lys Arg Tyr
 20 25 30
 ggc ctg ctg atg gcg gct gcc ctc ctg gaa ggc gct tcg gtc gga ccc 143
 Gly Leu Leu Met Ala Ala Ala Leu Leu Glu Gly Ala Ser Val Gly Pro
 35 40 45
 ctc gtc aag ctc gcc gtg gaa ttt gac cca agc atc ctg gtg acg gcg 191
 Leu Val Lys Leu Ala Val Glu Phe Asp Pro Ser Ile Leu Val Thr Ala
 50 55 60
 ttc gtg ggg act gcc atc gcg ttc gcg tgc ttc tcc ggc gcg cca tgg 239
 Phe Val Gly Thr Ala Ile Ala Phe Ala Cys Phe Ser Gly Ala Pro Trp
 65 70 75
 tgg cag gcc agg gag tac ctc tac ctg ggc ggc tgc tct cgt cga ggc 287
 Trp Gln Ala Arg Glu Tyr Leu Tyr Leu Gly Gly Cys Ser Arg Arg Gly
 80 85 90 95
 tct cca tcc tgc tct ggc tgc agc tcg ccg cct cca tct tcg gca ctc 335
 Ser Pro Ser Cys Ser Gly Cys Ser Ser Pro Pro Pro Ser Ser Ala Leu
 100 105 110
 cgc aac agc ttc atg ttc gag gtc tac ttc ggc ctg ctc att ctt ctg 383
 Arg Asn Ser Phe Met Phe Glu Val Tyr Phe Gly Leu Leu Ile Leu Leu
 115 120 125
 ggc ta 388
 Gly

<210> 28
 <211> 128
 <212> PRT
 <213> Zea mays

<400> 28
 Trp Asn Ile Gly Gly Thr Leu Thr Met Leu Gly Cys Val Gly Ser Ile
 1 5 10 15

Ala Trp Leu Phe Ser Val Pro Val Tyr Glu Glu Arg Lys Arg Tyr Gly
 20 25 30

Leu Leu Met Ala Ala Ala Leu Leu Glu Gly Ala Ser Val Gly Pro Leu
 35 40 45

Val Lys Leu Ala Val Glu Phe Asp Pro Ser Ile Leu Val Thr Ala Phe
 50 55 60

Val Gly Thr Ala Ile Ala Phe Ala Cys Phe Ser Gly Ala Pro Trp Trp
 65 70 75 80

Gln Ala Arg Glu Tyr Leu Tyr Leu Gly Gly Cys Ser Arg Arg Gly Ser
 85 90 95

Pro Ser Cys Ser Gly Cys Ser Ser Pro Pro Pro Ser Ser Ala Leu Arg
 100 105 110

Asn Ser Phe Met Phe Glu Val Tyr Phe Gly Leu Leu Ile Leu Leu Gly
 115 120 125

<210> 29

<211> 1737

<212> DNA

<213> Solanum tuberosum

<220>

<221> promoter

<222> (1)..(1737)

<223> patatin promoter

<400> 29

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aagcttatgt tgccatatag agtagtttgt gatggtatac ttcataaaact ttaacttatg 60
ttaaatttgt aatgataaaa tttttattgt aaattaaaaa ttacttataa aattgggcat 120
tataacatat gaaagacaaa ttgtgttaca tattttactt ttgactttaa tatgaatatt 180
tcaatttaaa tcattgtttt attttctctt tctttttaca ggtataaaaag gtgaaaattg 240
aagcaagatt gattgcaagc tatgtgtcac cacgttattg atactttgga agaattttt 300
acttatatgt ctttgttttag gagtaatatt tgatatgttt tagttagatt ttcttgtcat 360
ttatgcttta gtataatttt agttattttt attatatgat catgggtgaa ttttgataca 420
aatatttttg tcattaaata aattaattta tcacaacttg attactttca gtgacaaaaa 480
atgtattgtc gtagtaccct tttttgttga atatgaataa ttttttttat tttgtgacaa 540
ttgtaattgt cactacttat gataatatat agtgacatat atgtcgtcgg taaaagcaaa 600
cactttcagt gacaaaataa tagatttaat cacaaaatta ttaacctttt ttataataat 660
aaatttatcc ctaattttata catttaagga caaagtattt tttttatata taaaaaatag 720
tctttagtga cgatcgtagt gttgagtcta gaaatcataa tgttgaatct agaaaaatct 780
catgcagtgt aaaataaacc tcaaaaagga cgttcagtc atagaggggg tgtatgtgac 840
accccaacct cagcaaaaga aaacctccct tcaacaagga catttgcggt gctaaacaat 900
ttcaagtctc atcacacata tattttattat ataatactaa taaagaatag aaaaggaaaag 960
gtaaacatca ttaaatcgtc tttgtatatt ttttagtgaca actgattgac gaaatctttt 1020
tcgtcacaca aaatttttag tgacgaaaca tgatttatag atgatgaaat tatttgtccc 1080
tcataatcta atttgttgta gtgatcatta ctctttgtt tgttttatit gtcattgttag 1140
tccattaaaa aaaaatatct ctcttcttat gtacgtgaat gggtggaacg gatctattat 1200
ataatactaa taaagaatag aaaaaggaaa gtgagtgagg ttcgaggagg agaactctgtt 1260
taatatcaga gtcgatcatg tgtcaatttt atcgatatga ccctaacttc aactgagttt 1320
aaccaattcc gataaggcga gaaatatcat agtattgagt ctagaaaaat ctcattgttag 1380

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gtggggtaaa cctcagcaag gacgttgagt ccatagaggg ggggtgatgt gacaccccaa 1440
cctcagcaaa agaaaacctc ccctcaagaa ggacatttgc ggtgctaaac aattttcaagt 1500
ctcatcacac atatatatat attatataat actaataaat aatagaaaaa ggaaaggtaa 1560
acatcactaa cgacagttgc ggtgcaaact gagtgaggta ataaacatca ctaactttta 1620
ttggttatgt caaactcaaa gtaaaatttc tcaacttggt tacgtgccta tatataccat 1680
gcttgttata tgctcaaagc accaacaaaa tttaaaaaca ctttgaacat ttgcaaa 1737

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<210> 30

<211> 1317

<212> DNA

<213> *Triticum aestivum*

<220>

<221> promoter

<222> (1)..(1317)

<223> germin 9f-3.8 gene promoter

<400> 30

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gaattcaagc tatcactctc gaaccaagca cattgatgta aggtatcatt ggattccaga 60
tgtcgtgagt tccaagttgc tgaaacttga gaagatccat accgacgaca atggttcaga 120
tatgatgacc aagatattgc gaaaataagaa gctacaagca tgttgcaagg tagcgggcat 180
ggcggtgccc ccatcatgag tcggaggggg agatttgttg ggatatcctc ctcatgtggg 240
ttctgaggag atgaccattt gaggcctttt agccagccca aagagggtgca gaagcccact 300
acccattagg gttatgacct agggtcattt tggactttgc acatgagtgg atggggatgc 360
tttaccctcc atccagcagc caccaccaag ggtgacgaaa atcagttcat cctccaagag 420
agaagaagag agaaaaaccaa gagagcaagg gaagaagagg aagattgaag gaagaagaaa 480
agggagctcc tccccaaggt tgtgatggtc catatccact atcttgtctc cttcaaactt 540
cggttccacc atcttttggt agattgttct aatccctagt tcttgagccc caaatcttgt 600
tgtgttcac caagattcag aaatcttgat gtatgagatc ctctagtgtc gtctagagaa 660
gaatttgttg tatcccacat ttgataatag tgggaagagga tttgggtggc ttcggcccat 720
ggtttttccc ctcaagttga ggggttttcc acgtaaaatc tgggtgtctc ttgttgatgc 780
ttgggtgttg ccagaaactt actcctacca caagacacta ggggccagtt cttttgggaa 840
attctcccag aattgaccct ctcccagct tctcccagaa ttgtcactcc atttttcttt 900
acaattccta gctagttaag gtctaattag ttaggaattg taaaaaaata tcaagtggca 960
attctgggag aagctgggga ggggttcaat tctggaagaa ttgcccaaaa gaactggccc 1020
taggctgagg agtgtcttgc ctgctgctta acattttctg cctccatata tgttgttgca 1080
tatgtttcct tccgtgctaa gcaacgatcc ttgagttagt acatgatgtg gtgctgagat 1140
tactttgttt tcgctgcagt tatcagttaa ccacaagtgc atttgctgct taattcccaa 1200
caatatgcc acccgaactc atccaccata gctcagcagc aaccaccaat gccatagaca 1260
ctctcggtaa acaacctgta gcttatcagt ctagctaagc gtgctgcata gcaagca 1317

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<210> 31

<211> 959

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> promoter

<222> (1)..(959)

<223> CAB-2 promoter

<400> 31

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gaattcatgt gtgagggcaa ttagtgattg taaaaataaa attgtgtttt gtaaaaaact 60
tttactgtcg aaattattta gggatgatga aaaatcagta aactacgaat gatagcttaa 120
agagtttcta tcaaagtgat tgaggaatag tttgttgcaa attaaacctc taacaaaatg 180

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ttttctgttg tggtttttca tctctacaaa ttttgaattt tatgatgaat tagaaagata 240
gaatgagtta ctttagattt taaaagggtg ttcaagttaa caaaacagat tactagaatc 300
atgattaaaa atttacaagc tacatattgt ctaaaccaat gatgttgaac ataccagatg 360
atagtttttc agtgtttgaa caatcaattg gatagttttt atgtttctgc aaaatatgca 420
aataatcagt gtttttgagt ctttgcattt tgatttaaaa gcaaaaacaa ctgagtttca 480
aggttaaatt aattacatta ttcatgagat ttatcagggt agtggataaa ctgacaatgg 540
aatcaatggt attgtaaatt ggtagtgatg ttggacttct aatgttactc tctatgatgt 600
ttcggtcacg ggtatcacac tatctttact tttatttaaa ggaaagatca cacaaataag 660
ttatctctat tcagaactat taagctgctt ccaaaagact tgcaacatgt ggtctcgaaa 720
tgctttggct gcaatgaaaa aatcatagca aaagctagtg gactagagac tgccacataa 780
gaatagtaaa cgttaaaacc aaaatctcaa aaatccaatg agtaaagaga tatagattac 840
ttcatagata acaaacgtta ctcgcaattt tcctatataa tccaacccta cctaaccatt 900
ttcaatcact ctcaatcaca agttagtcac caaaaaaaaa aaaaacacaa aaagtttca 959

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<210> 32

<211> 445

<212> DNA

<213> Zea mays

<220>

<221> promoter

<222> (1)..(445)

<223> PPCZm1 promoter

<400> 32

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gaattccaaa aatagacacg gcaattttct tattcacaga aaaaatataa ctacaactaa 60
tccccagtc cacagggatt agggatcaat ctgcaaaact aaaagtactt ttacagttgt 120
acttggcatg agtcatgtga ccatgagaga ggcgcacggg tcagcaaagc aacataaaat 180
tctccaaacg ggccccgcca cacacgatca ccatcacccc cgggctcccc acccagtaca 240
aatagacacg cacactccca actccccacc catctccgcc gcgcacaccg cccaatcagc 300
caatctcttc ctctctctcc gctctcagac gagcagcggg tgccatcact ctccacttcc 360
cacgcccgtc gcgggctcgc aggcggcaga gaattgtctg tgccgcgggg tgggaatttg 420
attcggtcgg attccgtgcg ccgcg

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445

<210> 33

<211> 5455

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:
recombinant expression vector pUbiBI-1

<400> 33

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ggggatcctc tagagtcgac ctgcaggcgg ccgcactagt gattaggatt ccaacgcgag 60
ccaggacaag cgaggaacct tgcgtgcgag gcgaggccgc cccgctccga ttcgattcga 120
cgcgcaggcg caggcgcagg gatggacgcc ttctactcga cctcgtcggc ggcgggcgagc 180
ggctggggcc acgactccct caagaacttc cgccagatct cccccgccgt gcagtccac 240
ctcaagctcg tttaacctgac tctatgcttt gcaactggcct catctgccgt ggggtgcttac 300
ctacacattg ccctgaacat cggcgggatg ctgacaatgc tcgcttgtgt cggaactatc 360
gcctggatgt tctcggtgcc agtctatgag gagaggaaga ggtttgggct gctgatgggt 420
gcagccctcc tggaaggggc ttcggttgga cctctgattg agcttgccat agactttgac 480
ccaagcatcc tcgtgacagg gtttgtcgga accgccatcg cttttgggtg cttctctggc 540
gcgcgccatca tcgccaagcg cagggagtac ctgtacctcg gtggcctgct ctcgctctggc 600
ctgtcgatcc tgctctggct gcagtttgtc acgtccatct ttggccactc ctctggcagc 660

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<211> 5598

<212> DNA

<213> Artificial sequence

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Tyr Asp Ser Leu Lys Asn Phe Arg Glu Ile Ser Pro Ala Val Gln Ser

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20	25	30	
cac ctc aag ctc gtt tac ctg acc cta tgc ttt gcc ctg gcc tca tct His Leu Lys Leu Val Tyr Leu Thr Leu Cys Phe Ala Leu Ala Ser Ser 35 40 45			144
gcc gtg ggt gct tac ctg cac att gcc ctg aac atc ggt ggg atg ctg Ala Val Gly Ala Tyr Leu His Ile Ala Leu Asn Ile Gly Gly Met Leu 50 55 60			192
aca atg ctc gcg tgt gtt gga acc atc gcc tgg atg ttc tct gtg cca Thr Met Leu Ala Cys Val Gly Thr Ile Ala Trp Met Phe Ser Val Pro 65 70 75 80			240
gtc tat gag gag agg aag agg ttt ggg ctg ctg atg ggt gca gcc ctc Val Tyr Glu Glu Arg Lys Arg Phe Gly Leu Leu Met Gly Ala Ala Leu 85 90 95			288
ctg gaa ggg gct tcg gtt gga cct ctg att gag ctt gcc ata gac ttt Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Glu Leu Ala Ile Asp Phe 100 105 110			336
gac cca agt atc ctc gtg aca ggg ttt gtc gga acc gcc atc gcc ttc Asp Pro Ser Ile Leu Val Thr Gly Phe Val Gly Thr Ala Ile Ala Phe 115 120 125			384
ggg tgc ttc tct ggc gcc gcc atc atc gcc aag cgc agg gag tac ctg Gly Cys Phe Ser Gly Ala Ala Ile Ile Ala Lys Arg Arg Glu Tyr Leu 130 135 140			432
tac ctc ggt ggt ctg ctc tcc tcc ggc ctg tcg atc ctg ctc tgg ctg Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile Leu Leu Trp Leu 145 150 155 160			480
cag ttt gcc acg tcc atc ttt ggc cac tcc tct ggc agc ttc atg ttt Gln Phe Ala Thr Ser Ile Phe Gly His Ser Ser Gly Ser Phe Met Phe 165 170 175			528
gag gtt tac ttt ggc ctg ttg atc ttc ctg gga tac atg gtg tac gac Glu Val Tyr Phe Gly Leu Leu Ile Phe Leu Gly Tyr Met Val Tyr Asp 180 185 190			576
acg cag gag atc atc gag agg gcg cac cac ggc gac atg gat tac atc Thr Gln Glu Ile Ile Glu Arg Ala His His Gly Asp Met Asp Tyr Ile 195 200 205			624
aag cac gcg ctc acc ctc ttc acc gac ttc gtc gcc gtt ctc gtc cgc Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val Ala Val Leu Val Arg 210 215 220			672
gtc ctc atc atc atg ctc aag aac gca ggc gac aag tcg gag gac aag Val Leu Ile Ile Met Leu Lys Asn Ala Gly Asp Lys Ser Glu Asp Lys 225 230 235 240			720
aag aag agg aag agg ggg tcc tga Lys Lys Arg Lys Arg Gly Ser 245			744

<210> 38
 <211> 247
 <212> PRT
 <213> Triticum aestivum

<400> 38

Met	Asp	Ala	Phe	Tyr	Ser	Thr	Ser	Ser	Ala	Ala	Ala	Ser	Gly	Trp	Gly	1	5	10	15
Tyr	Asp	Ser	Leu	Lys	Asn	Phe	Arg	Glu	Ile	Ser	Pro	Ala	Val	Gln	Ser	20	25	30	
His	Leu	Lys	Leu	Val	Tyr	Leu	Thr	Leu	Cys	Phe	Ala	Leu	Ala	Ser	Ser	35	40	45	
Ala	Val	Gly	Ala	Tyr	Leu	His	Ile	Ala	Leu	Asn	Ile	Gly	Gly	Met	Leu	50	55	60	
Thr	Met	Leu	Ala	Cys	Val	Gly	Thr	Ile	Ala	Trp	Met	Phe	Ser	Val	Pro	65	70	75	80
Val	Tyr	Glu	Glu	Arg	Lys	Arg	Phe	Gly	Leu	Leu	Met	Gly	Ala	Ala	Leu	85	90	95	
Leu	Glu	Gly	Ala	Ser	Val	Gly	Pro	Leu	Ile	Glu	Leu	Ala	Ile	Asp	Phe	100	105	110	
Asp	Pro	Ser	Ile	Leu	Val	Thr	Gly	Phe	Val	Gly	Thr	Ala	Ile	Ala	Phe	115	120	125	
Gly	Cys	Phe	Ser	Gly	Ala	Ala	Ile	Ile	Ala	Lys	Arg	Arg	Glu	Tyr	Leu	130	135	140	
Tyr	Leu	Gly	Gly	Leu	Leu	Ser	Ser	Gly	Leu	Ser	Ile	Leu	Leu	Trp	Leu	145	150	155	160
Gln	Phe	Ala	Thr	Ser	Ile	Phe	Gly	His	Ser	Ser	Gly	Ser	Phe	Met	Phe	165	170	175	
Glu	Val	Tyr	Phe	Gly	Leu	Leu	Ile	Phe	Leu	Gly	Tyr	Met	Val	Tyr	Asp	180	185	190	
Thr	Gln	Glu	Ile	Ile	Glu	Arg	Ala	His	His	Gly	Asp	Met	Asp	Tyr	Ile	195	200	205	
Lys	His	Ala	Leu	Thr	Leu	Phe	Thr	Asp	Phe	Val	Ala	Val	Leu	Val	Arg	210	215	220	
Val	Leu	Ile	Ile	Met	Leu	Lys	Asn	Ala	Gly	Asp	Lys	Ser	Glu	Asp	Lys	225	230	235	240
Lys	Lys	Arg	Lys	Arg	Gly	Ser	245												

<210> 39
 <211> 1293
 <212> DNA
 <213> Hordeum vulgare

<220>
 <221> CDS
 <222> (173)..(1126)
 <223> coding for Hordeum vulgare subsp. vulgare syntaxin
 (Ror2)

<400> 39
 gtaactaacc ccttcttct ccttgtcca ctccgcttct ccccatccaa gaaacagcgc 60
 caacagctcc acccatcgag gagaatcaag aaaccgcgcc ggcgtggtga tcaaggacat 120
 ccatcgatcg atcgaccgac cctgccttgc ctgagtcaac ccggcggcag cc atg aac 178
 Met Asn
 1
 aac ctc ttc tcg agc tcg tgg aag cgg gcg ggc gcg ggg ggc gac ggg 226
 Asn Leu Phe Ser Ser Ser Trp Lys Arg Ala Gly Ala Gly Gly Asp Gly
 5 10 15
 gac ctg gag tcg ggc ggc ggc ggc gtg gag atg acg gcg ccg ccg ggc 274
 Asp Leu Glu Ser Gly Gly Gly Gly Val Glu Met Thr Ala Pro Pro Gly
 20 25 30
 gcc gcg gcg ggg gcg agc ctg gac cgc ttc ttc gag gac gtg gag tcg 322
 Ala Ala Ala Gly Ala Ser Leu Asp Arg Phe Phe Glu Asp Val Glu Ser
 35 40 45 50
 atc aag gac gac ctg cgg gag ctg gag cgg atc cag cgc tcc ctc cac 370
 Ile Lys Asp Asp Leu Arg Glu Leu Glu Arg Ile Gln Arg Ser Leu His
 55 60 65
 gac ggc aac gag tcg ggc aag tcg ctc cac gac gcg tcg gcg gtg cgc 418
 Asp Gly Asn Glu Ser Gly Lys Ser Leu His Asp Ala Ser Ala Val Arg
 70 75 80
 gcg ctc cgc tcc cgc atg gac gcc gac gtg gcc gcc gcc atc aag aag 466
 Ala Leu Arg Ser Arg Met Asp Ala Asp Val Ala Ala Ala Ile Lys Lys
 85 90 95
 gcc aag gtg gtg aag ttg cgg ctc gag tcg ctc gac cgc gcc aac gcc 514
 Ala Lys Val Val Lys Leu Arg Leu Glu Ser Leu Asp Arg Ala Asn Ala
 100 105 110
 gcc aac cgg tcc gtg gcc ggg tgc ggg ccg ggg tcg tcc acg gac cgc 562
 Ala Asn Arg Ser Val Ala Gly Cys Gly Pro Gly Ser Ser Thr Asp Arg
 115 120 125 130
 acc cgc acc tcc gtc gtg gcc ggg ctg cgc aag aag ctg cgg gat gcc 610
 Thr Arg Thr Ser Val Val Ala Gly Leu Arg Lys Lys Leu Arg Asp Ala
 135 140 145

atg gag tcc ttc tcc tcc ctc cgc tcc cgc atc acc tcc gag tac cgg 658
 Met Glu Ser Phe Ser Ser Leu Arg Ser Arg Ile Thr Ser Glu Tyr Arg
 150 155 160

gaa acc gtg gcc cgc cgc tac ttc acg gtg acg ggg tcc cag ccc gac 706
 Glu Thr Val Ala Arg Arg Tyr Phe Thr Val Thr Gly Ser Gln Pro Asp
 165 170 175

gag gcc acg ctg gac acg ctg gcg gag acg ggg gag ggg gag cgg ctc 754
 Glu Ala Thr Leu Asp Thr Leu Ala Glu Thr Gly Glu Gly Glu Arg Leu
 180 185 190

ctg cag cgc gcc atc gcg gag cag cag ggg aga ggg gag gtg ctg ggc 802
 Leu Gln Arg Ala Ile Ala Glu Gln Gln Gly Arg Gly Glu Val Leu Gly
 195 200 205 210

gtg gtg gcg gag atc cag gag cgg cac ggc gcc gtg gcg gac ctg gag 850
 Val Val Ala Glu Ile Gln Glu Arg His Gly Ala Val Ala Asp Leu Glu
 215 220 225

cgg tcc ctg ctg gag ctg cag cag gtg ttc aac gac atg gcc gtg ctg 898
 Arg Ser Leu Leu Glu Leu Gln Gln Val Phe Asn Asp Met Ala Val Leu
 230 235 240

gtg gcg gcg cag ggg gag cag ctg gac gac atc gag ggc cac gtc ggg 946
 Val Ala Ala Gln Gly Glu Gln Leu Asp Asp Ile Glu Gly His Val Gly
 245 250 255

cgg gcg agg tgc ttc gtc gac cgc ggg cgc gag cag ctg cag gtg gca 994
 Arg Ala Arg Ser Phe Val Asp Arg Gly Arg Glu Gln Leu Gln Val Ala
 260 265 270

cgc aag cac cag aag agc tcc cgc aag tgg acc ttc atc ggc atc ggc 1042
 Arg Lys His Gln Lys Ser Ser Arg Lys Trp Thr Phe Ile Gly Ile Gly
 275 280 285 290

atc ctg ctc gtc gtc atc ctc atc atc gtc atc ccc atc gtg ctc aag 1090
 Ile Leu Leu Val Val Ile Leu Ile Ile Val Ile Pro Ile Val Leu Lys
 295 300 305

aac acc aac aag agc aac aac aac aac agc cag cag tagtggtagg 1136
 Asn Thr Asn Lys Ser Asn Asn Asn Asn Ser Gln Gln
 310 315

aacagcctgt ggatctgttg tctgtctctg atgatcctgg tcctggattg cttcctgggt 1196

gttgttggtg attgtctttt gtggaatttt ttgcgattgt aattactcca tccatgtggt 1256

tcgttgagcc actcgattat tatttcatga ctatata 1293

<210> 40

<211> 318

<212> PRT

<213> Hordeum vulgare

<400> 40

Met Asn Asn Leu Phe Ser Ser Ser Trp Lys Arg Ala Gly Ala Gly Gly
 1 5 10 15
 Asp Gly Asp Leu Glu Ser Gly Gly Gly Gly Val Glu Met Thr Ala Pro
 20 25 30
 Pro Gly Ala Ala Ala Gly Ala Ser Leu Asp Arg Phe Phe Glu Asp Val
 35 40 45
 Glu Ser Ile Lys Asp Asp Leu Arg Glu Leu Glu Arg Ile Gln Arg Ser
 50 55 60
 Leu His Asp Gly Asn Glu Ser Gly Lys Ser Leu His Asp Ala Ser Ala
 65 70 75 80
 Val Arg Ala Leu Arg Ser Arg Met Asp Ala Asp Val Ala Ala Ala Ile
 85 90 95
 Lys Lys Ala Lys Val Val Lys Leu Arg Leu Glu Ser Leu Asp Arg Ala
 100 105 110
 Asn Ala Ala Asn Arg Ser Val Ala Gly Cys Gly Pro Gly Ser Ser Thr
 115 120 125
 Asp Arg Thr Arg Thr Ser Val Val Ala Gly Leu Arg Lys Lys Leu Arg
 130 135 140
 Asp Ala Met Glu Ser Phe Ser Ser Leu Arg Ser Arg Ile Thr Ser Glu
 145 150 155 160
 Tyr Arg Glu Thr Val Ala Arg Arg Tyr Phe Thr Val Thr Gly Ser Gln
 165 170 175
 Pro Asp Glu Ala Thr Leu Asp Thr Leu Ala Glu Thr Gly Glu Gly Glu
 180 185 190
 Arg Leu Leu Gln Arg Ala Ile Ala Glu Gln Gln Gly Arg Gly Glu Val
 195 200 205
 Leu Gly Val Val Ala Glu Ile Gln Glu Arg His Gly Ala Val Ala Asp
 210 215 220
 Leu Glu Arg Ser Leu Leu Glu Leu Gln Gln Val Phe Asn Asp Met Ala
 225 230 235 240
 Val Leu Val Ala Ala Gln Gly Glu Gln Leu Asp Asp Ile Glu Gly His
 245 250 255
 Val Gly Arg Ala Arg Ser Phe Val Asp Arg Gly Arg Glu Gln Leu Gln
 260 265 270
 Val Ala Arg Lys His Gln Lys Ser Ser Arg Lys Trp Thr Phe Ile Gly
 275 280 285
 Ile Gly Ile Leu Leu Val Val Ile Leu Ile Ile Val Ile Pro Ile Val
 290 295 300

Leu Lys Asn Thr Asn Lys Ser Asn Asn Asn Asn Ser Gln Gln
 305 310 315

<210> 41

<211> 948

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(945)

<223> coding for Arabidopsis thaliana syntaxin 121
 (SYP121) / syntaxin-related protein (SYR1)
 (At3g11820)

<400> 41

atg gcg aat ccc gcg gga tca acc ggt ggt gtg aac ctc gac aag ttc	48
Met Ala Asn Pro Ala Gly Ser Thr Gly Gly Val Asn Leu Asp Lys Phe	
1 5 10 15	
ttc gaa gat gtt gaa tct gtg aaa gaa gag cta aag gag cta gat cgg	96
Phe Glu Asp Val Glu Ser Val Lys Glu Glu Leu Lys Glu Leu Asp Arg	
20 25 30	
ctc aac gaa aca ctc tct tca tgt cac gag cag agc aag acg ctt cac	144
Leu Asn Glu Thr Leu Ser Ser Cys His Glu Gln Ser Lys Thr Leu His	
35 40 45	
aat gct aaa gcc gtt aaa gat ctc cgg tct aaa atg gac ggt gac gtt	192
Asn Ala Lys Ala Val Lys Asp Leu Arg Ser Lys Met Asp Gly Asp Val	
50 55 60	
gga gtc gcg ttg aag aag gcg aag atg att aaa gtt aaa ctc gag gcg	240
Gly Val Ala Leu Lys Lys Ala Lys Met Ile Lys Val Lys Leu Glu Ala	
65 70 75 80	
cta gat cgt gcc aat gct gct aat cgg agt ctc cct ggc tgt gga cct	288
Leu Asp Arg Ala Asn Ala Ala Asn Arg Ser Leu Pro Gly Cys Gly Pro	
85 90 95	
ggt tct tcc tcc gat cga acc agg acc tct gtc ctc aat ggt ctc agg	336
Gly Ser Ser Ser Asp Arg Thr Arg Thr Ser Val Leu Asn Gly Leu Arg	
100 105 110	
aag aaa ttg atg gac tct atg gat agt ttc aac cga ttg agg gag ctt	384
Lys Lys Leu Met Asp Ser Met Asp Ser Phe Asn Arg Leu Arg Glu Leu	
115 120 125	
atc tcg tcc gag tat aga gaa act gta cag agg agg tac ttc acc gtc	432
Ile Ser Ser Glu Tyr Arg Glu Thr Val Gln Arg Arg Tyr Phe Thr Val	
130 135 140	
acc ggc gag aat ccg gat gaa cga acc cta gat cga ctg att tcc act	480
Thr Gly Glu Asn Pro Asp Glu Arg Thr Leu Asp Arg Leu Ile Ser Thr	
145 150 155 160	

gga gag agt gag aga ttc ttg cag aaa gca ata caa gaa caa gga aga 528
 Gly Glu Ser Glu Arg Phe Leu Gln Lys Ala Ile Gln Glu Gln Gly Arg
 165 170 175

gga agg gtg tta gac acc att aac gag att caa gaa agg cat gat gcg 576
 Gly Arg Val Leu Asp Thr Ile Asn Glu Ile Gln Glu Arg His Asp Ala
 180 185 190

gtt aaa gac att gag aag aat ctc agg gag ctt cac cag gtg ttt cta 624
 Val Lys Asp Ile Glu Lys Asn Leu Arg Glu Leu His Gln Val Phe Leu
 195 200 205

gac atg gcc gtg ctg gta gag cac cag gga gct cag ctt gat gac atc 672
 Asp Met Ala Val Leu Val Glu His Gln Gly Ala Gln Leu Asp Asp Ile
 210 215 220

gag agt cat gtg ggt cga gct agc tcc ttt atc aga ggc gga act gac 720
 Glu Ser His Val Gly Arg Ala Ser Ser Phe Ile Arg Gly Gly Thr Asp
 225 230 235 240

cag cta caa acc gct cgg gtt tac cag aag aac acg cga aaa tgg aca 768
 Gln Leu Gln Thr Ala Arg Val Tyr Gln Lys Asn Thr Arg Lys Trp Thr
 245 250 255

tgt att gcc att att att ctc atc atc atc ata act gtt gtg gtt ctt 816
 Cys Ile Ala Ile Ile Ile Leu Ile Ile Ile Ile Thr Val Val Val Leu
 260 265 270

gct gtt tta aaa ccg tgg aac aac agc agt ggc ggc ggc ggc ggt ggt 864
 Ala Val Leu Lys Pro Trp Asn Asn Ser Ser Gly Gly Gly Gly Gly Gly
 275 280 285

ggt ggt ggg ggt acc act gga gga agt caa cca aat tca ggg aca cca 912
 Gly Gly Gly Gly Thr Thr Gly Gly Ser Gln Pro Asn Ser Gly Thr Pro
 290 295 300

cca aat cct cct cag gca agg cgt cta ttg cgt tga 948
 Pro Asn Pro Pro Gln Ala Arg Arg Leu Leu Arg
 305 310 315

<210> 42

<211> 315

<212> PRT

<213> Arabidopsis thaliana

<400> 42

Met Ala Asn Pro Ala Gly Ser Thr Gly Gly Val Asn Leu Asp Lys Phe
 1 5 10 15

Phe Glu Asp Val Glu Ser Val Lys Glu Glu Leu Lys Glu Leu Asp Arg
 20 25 30

Leu Asn Glu Thr Leu Ser Ser Cys His Glu Gln Ser Lys Thr Leu His
 35 40 45

Asn Ala Lys Ala Val Lys Asp Leu Arg Ser Lys Met Asp Gly Asp Val
 50 55 60
 Gly Val Ala Leu Lys Lys Ala Lys Met Ile Lys Val Lys Leu Glu Ala
 65 70 75 80
 Leu Asp Arg Ala Asn Ala Ala Asn Arg Ser Leu Pro Gly Cys Gly Pro
 85 90 95
 Gly Ser Ser Ser Asp Arg Thr Arg Thr Ser Val Leu Asn Gly Leu Arg
 100 105 110
 Lys Lys Leu Met Asp Ser Met Asp Ser Phe Asn Arg Leu Arg Glu Leu
 115 120 125
 Ile Ser Ser Glu Tyr Arg Glu Thr Val Gln Arg Arg Tyr Phe Thr Val
 130 135 140
 Thr Gly Glu Asn Pro Asp Glu Arg Thr Leu Asp Arg Leu Ile Ser Thr
 145 150 155 160
 Gly Glu Ser Glu Arg Phe Leu Gln Lys Ala Ile Gln Glu Gln Gly Arg
 165 170 175
 Gly Arg Val Leu Asp Thr Ile Asn Glu Ile Gln Glu Arg His Asp Ala
 180 185 190
 Val Lys Asp Ile Glu Lys Asn Leu Arg Glu Leu His Gln Val Phe Leu
 195 200 205
 Asp Met Ala Val Leu Val Glu His Gln Gly Ala Gln Leu Asp Asp Ile
 210 215 220
 Glu Ser His Val Gly Arg Ala Ser Ser Phe Ile Arg Gly Gly Thr Asp
 225 230 235 240
 Gln Leu Gln Thr Ala Arg Val Tyr Gln Lys Asn Thr Arg Lys Trp Thr
 245 250 255
 Cys Ile Ala Ile Ile Ile Leu Ile Ile Ile Ile Thr Val Val Val Leu
 260 265 270
 Ala Val Leu Lys Pro Trp Asn Asn Ser Ser Gly Gly Gly Gly Gly Gly
 275 280 285
 Gly Gly Gly Gly Thr Thr Gly Gly Ser Gln Pro Asn Ser Gly Thr Pro
 290 295 300
 Pro Asn Pro Pro Gln Ala Arg Arg Leu Leu Arg
 305 310 315

<210> 43

<211> 1275

<212> DNA

<213> Hordeum vulgare

<220>

<221> CDS

<222> (80)...(1006)

<223> coding for *Hordeum vulgare* subsp. *vulgare* SNAP-34

<400> 43

ggccccctcca cccacaccca cccagtcgct gcggatactt gattctgcta ctccggccagc 60

gatcgatctc gcctccgcc atg agc gcc acc agg ccc tcc ttc ttc ccc tcc 112
 Met Ser Ala Thr Arg Pro Ser Phe Phe Pro Ser
 1 5 10

aac aac aac agg aac aag ccc gcc acc cgg aac ccc ttc gac tcc gac 160
 Asn Asn Asn Arg Asn Lys Pro Ala Thr Arg Asn Pro Phe Asp Ser Asp
 15 20 25

tcg gac gac gac ggc ggc atg gcc cgg cgc ggc ccg gcg cgg gcc tcg 208
 Ser Asp Asp Asp Gly Gly Met Ala Arg Arg Gly Pro Ala Arg Ala Ser
 30 35 40

tcc gtc ccg acc ccc gcc gcg ggg ccg gcc agg gcc tcc tcg gcc ccg 256
 Ser Val Pro Thr Pro Ala Ala Gly Pro Ala Arg Ala Ser Ser Ala Pro
 45 50 55

atc ccc gcc gac gag gcg gac cag cgg ggc gcc ctg ttc ggc gcg ggc 304
 Ile Pro Ala Asp Glu Ala Asp Gln Arg Gly Ala Leu Phe Gly Ala Gly
 60 65 70 75

ccc gcg ccg tcc ggc ttc gcg tcc tcc tcc tcc gcg gcc gcc agg ggc 352
 Pro Ala Pro Ser Gly Phe Ala Ser Ser Ser Ser Ala Ala Ala Arg Gly
 80 85 90

cgg tac agg aac gac ttc cgc gac tcg ggc ggc gtg gag gcg cag tcc 400
 Arg Tyr Arg Asn Asp Phe Arg Asp Ser Gly Gly Val Glu Ala Gln Ser
 95 100 105

gtg cag gag ctc gag ggc tac gcg gcc tac aag gcc gag gag acc acg 448
 Val Gln Glu Leu Glu Gly Tyr Ala Ala Tyr Lys Ala Glu Glu Thr Thr
 110 115 120

cgc cgg gtc gac ggc tgc ctc cgg gtc gcc gag gag atg cgg gac acc 496
 Arg Arg Val Asp Gly Cys Leu Arg Val Ala Glu Glu Met Arg Asp Thr
 125 130 135

gcg tca aag acc ctg ctc cag gtg cac cag cag ggc cag cag atc agg 544
 Ala Ser Lys Thr Leu Leu Gln Val His Gln Gln Gly Gln Gln Ile Arg
 140 145 150 155

cgc acc cac gcc atg gcc gtc gac atc gac cag gat ctc tcc agg ggg 592
 Arg Thr His Ala Met Ala Val Asp Ile Asp Gln Asp Leu Ser Arg Gly
 160 165 170

gaa aag cta cta ggt gat ctt ggt ggt ttg ttt tcc aag aag tgg aag 640
 Glu Lys Leu Leu Gly Asp Leu Gly Gly Leu Phe Ser Lys Lys Trp Lys
 175 180 185

cca aag aag aac ggc gca atc agg ggc cct atg ctg acc aga gac gat 688
 Pro Lys Lys Asn Gly Ala Ile Arg Gly Pro Met Leu Thr Arg Asp Asp
 190 195 200

tcc ttc ata cgc aag ggc agc cat atg gag cag agg cat aaa ctg ggg 736
 Ser Phe Ile Arg Lys Gly Ser His Met Glu Gln Arg His Lys Leu Gly
 205 210 215

ctg tca gat cgt ccg cat cga tcc aat gca cgc cag ttc cta tct gaa 784
 Leu Ser Asp Arg Pro His Arg Ser Asn Ala Arg Gln Phe Leu Ser Glu
 220 225 230 235

ccc aca tca ggc ctt gag aaa gtc gag gtg gag aag gca aag cag gat 832
 Pro Thr Ser Gly Leu Glu Lys Val Glu Val Glu Lys Ala Lys Gln Asp
 240 245 250

gat ggc ctg tct gac ctt agc gac ata ctg aca gag ttg aaa gga atg 880
 Asp Gly Leu Ser Asp Leu Ser Asp Ile Leu Thr Glu Leu Lys Gly Met
 255 260 265

gcc att gac atg gga act gag att gag ggg caa aca aag gat ctt ggt 928
 Ala Ile Asp Met Gly Thr Glu Ile Glu Gly Gln Thr Lys Asp Leu Gly
 270 275 280

cat gcg gag aag gac ttt gac gaa ctt aac tac agg gtc aag ggg gca 976
 His Ala Glu Lys Asp Phe Asp Glu Leu Asn Tyr Arg Val Lys Gly Ala
 285 290 295

aac gct cga aca cgt cgc ctg ctt ggc aga taggcaagaa gcatatgttg 1026
 Asn Ala Arg Thr Arg Arg Leu Leu Gly Arg
 300 305

ttcaccagag gattctgtga cactccttat cttctgcatt tgctttcgtg ggctgttaat 1086

tcagatcatt ttgtgcataa aactctgggt aggaaggctt gttggggagt tgtatcaggg 1146

tttattgtgt atatacgcta gacgggcggt tcgttttcta tgttgcagtt gtactacatt 1206

tgctatggac agtagatacg tttgtattcg gttttcttgt tttgcaatcg ctatgctgca 1266

ggaaagcac 1275

<210> 44

<211> 309

<212> PRT

<213> Hordeum vulgare

<400> 44

Met Ser Ala Thr Arg Pro Ser Phe Phe Pro Ser Asn Asn Asn Arg Asn
 1 5 10 15

Lys Pro Ala Thr Arg Asn Pro Phe Asp Ser Asp Ser Asp Asp Asp Gly
 20 25 30

Gly Met Ala Arg Arg Gly Pro Ala Arg Ala Ser Ser Val Pro Thr Pro
 35 40 45

Ala Ala Gly Pro Ala Arg Ala Ser Ser Ala Pro Ile Pro Ala Asp Glu
 50 55 60
 Ala Asp Gln Arg Gly Ala Leu Phe Gly Ala Gly Pro Ala Pro Ser Gly
 65 70 75 80
 Phe Ala Ser Ser Ser Ser Ala Ala Ala Arg Gly Arg Tyr Arg Asn Asp
 85 90 95
 Phe Arg Asp Ser Gly Gly Val Glu Ala Gln Ser Val Gln Glu Leu Glu
 100 105 110
 Gly Tyr Ala Ala Tyr Lys Ala Glu Glu Thr Thr Arg Arg Val Asp Gly
 115 120 125
 Cys Leu Arg Val Ala Glu Glu Met Arg Asp Thr Ala Ser Lys Thr Leu
 130 135 140
 Leu Gln Val His Gln Gln Gly Gln Gln Ile Arg Arg Thr His Ala Met
 145 150 155 160
 Ala Val Asp Ile Asp Gln Asp Leu Ser Arg Gly Glu Lys Leu Leu Gly
 165 170 175
 Asp Leu Gly Gly Leu Phe Ser Lys Lys Trp Lys Pro Lys Lys Asn Gly
 180 185 190
 Ala Ile Arg Gly Pro Met Leu Thr Arg Asp Asp Ser Phe Ile Arg Lys
 195 200 205
 Gly Ser His Met Glu Gln Arg His Lys Leu Gly Leu Ser Asp Arg Pro
 210 215 220
 His Arg Ser Asn Ala Arg Gln Phe Leu Ser Glu Pro Thr Ser Gly Leu
 225 230 235 240
 Glu Lys Val Glu Val Glu Lys Ala Lys Gln Asp Asp Gly Leu Ser Asp
 245 250 255
 Leu Ser Asp Ile Leu Thr Glu Leu Lys Gly Met Ala Ile Asp Met Gly
 260 265 270
 Thr Glu Ile Glu Gly Gln Thr Lys Asp Leu Gly His Ala Glu Lys Asp
 275 280 285
 Phe Asp Glu Leu Asn Tyr Arg Val Lys Gly Ala Asn Ala Arg Thr Arg
 290 295 300
 Arg Leu Leu Gly Arg
 305

<210> 45
 <211> 6
 <212> PRT

<213> Consensus

<220>

<221> misc_feature

<222> (2)..(2)

<223> l or i

<220>

<221> misc_feature

<222> (4)..(4)

<223> Xaa can be any naturally occurring amino acid

<400> 45

His Leu Lys Xaa Val Tyr

1

5

<210> 46

<211> 7

<212> PRT

<213> Consensus

<220>

<221> misc_feature

<222> (2)..(2)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature

<222> (5)..(5)

<223> y or f

<220>

<221> misc_feature

<222> (6)..(6)

<223> Xaa can be any naturally occurring amino acid

<400> 46

Ala Xaa Gly Ala Tyr Xaa His

1

5

<210> 47

<211> 4

<212> PRT

<213> Consensus

<400> 47

Asn Ile Gly Gly

1

<210> 48

<211> 8

<212> PRT

<213> Consensus

<220>
 <221> misc_feature
 <222> (2)..(2)
 <223> v or p

<220>
 <221> misc_feature
 <222> (3)..(3)
 <223> y or f

<220>
 <221> misc_feature
 <222> (5)..(5)
 <223> e or q

<220>
 <221> misc_feature
 <222> (6)..(6)
 <223> r or q

<400> 48
 Pro Val Tyr Glu Glu Arg Lys Arg
 1 5

<210> 49
 <211> 8
 <212> PRT
 <213> Consensus

<220>
 <221> misc_feature
 <222> (1)..(1)
 <223> e or q

<220>
 <221> misc_feature
 <222> (3)..(3)
 <223> a or s

<220>
 <221> misc_feature
 <222> (5)..(5)
 <223> v or i

<400> 49
 Glu Gly Ala Ser Val Gly Pro Leu
 1 5

<210> 50
 <211> 5
 <212> PRT
 <213> Consensus

<220>

<221> misc_feature
 <222> (3)..(3)
 <223> s or g

<220>
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 <222> (4)..(4)
 <223> l or i

<220>
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 <222> (5)..(5)
 <223> i or l

<400> 50
 Asp Pro Ser Leu Ile
 1 5

<210> 51
 <211> 11
 <212> PRT
 <213> Consensus

<220>
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 <222> (2)..(2)
 <223> g or a

<220>
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 <222> (4)..(4)
 <223> a or s

<220>
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 <222> (5)..(5)
 <223> l or i

<220>
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 <222> (8)..(8)
 <223> a or g

<220>
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 <222> (11)..(11)
 <223> s or t

<400> 51
 Val Gly Thr Ala Leu Ala Phe Ala Cys Phe Ser
 1 5 10

<210> 52
 <211> 6
 <212> PRT

<213> Consensus

<220>

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<222> (3)..(3)

<223> y or f

<400> 52

Tyr Leu Tyr Leu Gly Gly

1

5

<210> 53

<211> 7

<212> PRT

<213> Consensus

<400> 53

Glu Tyr Leu Tyr Leu Gly Gly

1

5

<210> 54

<211> 11

<212> PRT

<213> Consensus

<220>

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<222> (2)..(2)

<223> l or v

<220>

<221> misc_feature

<222> (5)..(5)

<223> g or w

<220>

<221> misc_feature

<222> (7)..(7)

<223> s or t

<220>

<221> misc_feature

<222> (8)..(8)

<223> i or m

<220>

<221> misc_feature

<222> (10)..(10)

<223> l or m

<400> 54

Leu Leu Ser Ser Gly Leu Ser Ile Leu Leu Trp

1

5

10

<210> 55
 <211> 7
 <212> PRT
 <213> Consensus

<220>
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 <222> (4)..(4)
 <223> Xaa can be any naturally occurring amino acid

<220>
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 <222> (5)..(5)
 <223> i or v

<220>
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 <222> (6)..(6)
 <223> i or v

<400> 55
 Asp Thr Gly Xaa Ile Ile Glu
 1 5

<210> 56
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 <212> DNA
 <213> Artificial sequence

<220>
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 <222> (1)..(24)
 <223> BI1-sense primer

<400> 56
 atggacgcct tctactcgac ctcg

24

<210> 57
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> (1)..(20)
 <223> BI1-antisense primer

<400> 57
 gccagagcag gatcgacgcc

20

<210> 58
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
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 <222> (1)..(21)
 <223> UBI-sense primer

<400> 58
 ccaagatgca gatcttcgtg a

21

<210> 59
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 <212> DNA
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> (1)..(21)
 <223> UBI-antisense primer

<400> 59
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21

<210> 60
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 <212> DNA
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<220>
 <221> misc_feature
 <222> (1)..(26)
 <223> BI1VL sense primer

<400> 60
 ggattcaacg cgagcgcagg acaagc

26

<210> 61
 <211> 26
 <212> DNA
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> (1)..(26)
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<400> 61
 gtcgacgcgg tgacggtatc tacatg

26

<210> 62
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<220>
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<222> (1)..(18)
<223> M13-fwd primer

<400> 62
gtaaaacgac ggccagtg

18

<210> 63
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> (1)..(19)
<223> M13-rev primer

<400> 63
ggaaacagct atgaccatg

19